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Result
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Match
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       262574 seqs, 29422922 residues
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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US-08-883-515-4
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US-08-98120-426-4
US-08-99-120-426-4
US-09-134-001C-3034
US-09-134-001C-3477
US-09-134-001C-3477
US-09-134-001C-3945
US-08-91-454-2
US-08-91-454-7
US-08-91-454-7
US-09-128-4
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US-09-32-4338-7
US-09-128-4
US-09-32-6208-106
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US-08-935-450-4
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US-08-935-450-4
US-09-134-001C-5513
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         Sequence 4834, Ap
Sequence 2, Appli
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Sequence 124, Appli
Sequence 1124, Appli
Sequence 3034, Ap
Sequence 3477, Ap
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Sequence 30, Appli
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on US/08987146    Paul L.   Robert B.   Pamela K.   May     Jr., Paul R.   Streptococcus	54.2%; 54.3%; 34tive 3; TDCQALACES                 TDGQALNLS MGGGTCTGA                   MGGGTGTGTGA                 MGGGTGTGTA               MGGGTGTGA	NHB KO H OA	396 2647 2647 2547 345 345 270 459 449 458 458 458 641 458 641 458 641 458 641 458 641 458 641 458 641 458
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Pneumon1ae	54.2%; Score 480; DB 4; Lengt; imilarity 54.3%; Pred. No. 2.8e-47; Conservative 33; Mismatches 47; Ind LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKDELG	AMINO ACID DIAGNOSTIC ,001C	US-08-861-774E-8 US-08-583-562B-8 US-08-79-113-8 PCT-US95-03866-3 US-09-113-001C-3 US-09-113-013-881-6 US-09-428-17-33-2 US-09-428-517-3 13-08-618-485B-1 5177002-1 5177002-1 517702-2 US-08-822-619-5 PCT-US95-04075-5 US-08-836-567-10 US-09-320-878-2
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

Eli Lilly and Company

TITLE OF INVENTION:

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                                                         ; ORGANISM: Streptococcus pneumoniae US-09-120-426-2
                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 419
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Best Local Similarity
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APPLICANT: Fueyo, Joanna Lynn
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09120426 Patent No. 6197300
                 Query Match
Best Local Similarity
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/120,426
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 60/055,720
EARLIER FILING DATE: 1997-08-12
                                                                                                                                                                                                                                                              APPLICANT: Lonetto, Michael APPLICANT: Pearce, Kenneth TITLE OF INVENTION: ftsz
FILE REFERENCE: GM10068
                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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                                                                                              TYPE: PRT
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/987,146 FILING DATE: December 8, 1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: X-
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52.6%; Pred. No. 1.8e-46;
52. Mismatches 47;
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   Score 472; DB 4;
Pred. No. 2.6e-46;
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                     Length 419;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: WI
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                                                                                                                                   159 EALYGSDMVFVTAGMGGGTGTGAAPVIAGIAKAMGILTVGIATTPFSFEGRRTVQAQEG 218
                                                       219 LASLRDNVDTLIVIPNDKLLTAVSQSTPVTEAFNLADDILRQGVRGISDIITIPGLVNV 277
                                                                              98 DMVFITAGMGGGSGTGAAPVIARIAKDLGALTVGVVTRPFGFEGSKRGQFAVEGINQLRE 157
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                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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VENTION: PLANT CHLOROPLAST DIVISION GENES
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                                                                                                                                                                                                                                                                                                                52.3%; Score 463; DB 2; Length 437; 49.7%; Pred. No. 3e-45;
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                                                                                                                                                                                                                                                                                                 Mismatches
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US-09-120-426-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-883-515-2
                                                                                                                                                     APPLICANT: Fueyo, Joanna Lyn
APPLICANT: Lonetto, Michael
APPLICANT: Pearce, Kenneth
TITLE OF INVENTION: ftsz
FILE REFERENCE: GM10068
SEQ ID NO 4
LENGTH: 223
                                                                                                                                                                                                                                                                             Sequence 4, Application US/09120426 Patent No. 6197300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                   NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                          CURRENT APPLICATION NUMBER: US/09/120,426
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 60/055,720
EARLIER FILING DATE: 1997-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Seby, Nicholas J.
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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CITY: Madison
STATE: WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 ALKGSDLVFITAGMGGGTGSGAAPVVAQISKDAGYLTVGVVTYPFSFEGRKRSLQALEAI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 SSGLQSVDFYAINTDSQALLQFSAENPLQIGELLTRGLGTGGNPLLGEQAAEESKDAIAN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
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                                                                                                                                                                                                                                                                                                                                                                                                   EKLQKNVDTLIVIPNDRLLDIADEQTPLQDAFLLADDVLRQGVQGISDIITIPGLVNV 271
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VENTION: PLANT CHLOROPLAST DIVISION GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                 Joanna Lynn
o, Michael A.
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US-08-961-083-124
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US-08-961-083-124
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                                                                                                                                     Matches
                                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 Key
CITY: Rockville
                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                   105 FRSEGPNRTRLANAGVKELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 ADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                165 GVTDLIVRPGLINL 178
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61 GITDLITNPGLINL 74
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                                                                                                                                     38;
                                                                 1 FGFEGSKRGQFAVEGINQLREHVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLRQGVQ 60
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                                                                                                                                                                                                                                                                                   283 amino acids
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                                                                                                                                                                                                                                                                                                                                            (301
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                                                                                                                                   Conservative
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53.6%;
                                                                                                                                 22.1%; Score 196; DB 4;
51.4%; Pred. No. 1.3e-14;
tive 14; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae Antigens and Vaccines 452
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                                                                                                                                                                                                                                                                                                                           124:
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                                                                                                                                                                   4; Length 283;
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                                                                                                                                   22;
                                                                                                                                   Indels
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RESULT 8

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; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4951, Application US/09134001C
PATENT NO. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4951
LENGTH: 388
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CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REFERENCE: GC394-PCT
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5674
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73 TGGLGP--
                                         71 TGGMGGGTCTGAAPVVASVARELG--ILT----VGVVSTPFRSEGPNRTRLANAGVKELA 124
                                                                                        24
                                                                                                                             11 VANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDSNMLFI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ---GLGAGSKPELGKRSAEQQKVDIQRMLQDSNMLFITGGMGGGTCTGAAPVVASVAREL
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                                                                                                                                                                          Conservative
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-TKDDLTKHTVAKVLGKNLVTDEASLNFIKNYFKEQGQDMT---
                                                                                                                                                                                           8.9%; Score 79; DB 4; Length 388; 23.5%; Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.2%; Score 90.5; DB 21.4%; Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                   32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                          48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                       24;
  -SNNKQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                       Gaps
                                                                                   72
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; SOFTWARE: FastSEQ for W.
; SEQ ID NO 11
; LENGTH: 271
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-189-527-11
                                       QΥ
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                                                                                   밁
                                                                                                                           QΥ
                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3034
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US-09-134-001C-3034
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US-09-189-527-11
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                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3034
LENGTH: 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3034, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                       Matches
                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09189527A Patent No. 6387639
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/189,527A CURRENT FILING DATE: 1998-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: SLK98-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JOSEP O. Dalmau
APPLICANT: Myrna R. Rosenfeld
TITLE OF INVENTION: Ma Family Polypeptides
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                   214 ILEGTTASVPPQGGRKHPNQELIQI----DTTNILFILGGAFDG-----IDEVIKRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 KYVDTLIVVPNQNLLA 140
                                            94 GILTYGYVSTPFRSEGPNRTRLANAGVKELAKY-----
                                                                                                                           34 ITKGLGAGSKPELGKRSAEQQKVDIQRMLQDSNMLFITGGMGGGTCTGAAPVVASVAREL
                                                                                                                                                                       42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 VARE------LGILTVGVVSTPFRSEGPNRTRLANAGVKE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 GLGYVSSPGAGGRVSSHSALHLTR-----ITGPFVGTGNGTCASAPATHEIPETAS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 GLGAGSKPELGKRSAEQQKVDIQRMLQDSNMLFITG---GMGGGTCTGA-----APVVAS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
GEKVIGFASNE-ADKYDEEALLEQIRPEDLQSYGLIPEFIGRVPIVANLETLDVAALKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILRECCPSPRGRVLGLVGTG-----HGDSQRVASNRGRKE
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%;
                                                                                                                                                                                           8.6%; Score 76.5; D
23.0%; Pred. No. 1.7;
                                                                                                                                                                       25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                              DB 4; Length 422;
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                                                                                                                                                                       61;
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                                            -----VDTLIVVPNQNL 138
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                                                                                     262
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В

Db Db

1182 LETVEELVGRTDLLQRSTQLKPNSKAASLQIERLIEQFDGVNTK-EISQNHHLDEGFDLN 1240

1241 YLYPDARYSIENGHSFTGNY-----VVNNEQRDVGVITGSAIAKQYGEEGLPEDTILAYT 1295

RMLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEG-PNRTRLA-- 116

117 --NAGVKELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRP 173

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                                                                                                                                                                            ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3945
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US-09-134-001C-3945
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US-09-134-001C-3477
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Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PRIOR TILING DATE: 1997-08-14
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3945
LENGTH: 1529
TYPE: PRT
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3477
LENGTH: 327
TYPE: PRT
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                                                                                                    Query Match
Best Local
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                                                                          Match 8.4%; Score 74; DB Local Similarity 22.9%; Pred. No. 21; es 41; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 VKTIGLRSTRIQSDTGEIYTLPNGMISEIVNYSATDVSPIVMIPISPNENYKVIEEKLLT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 ML-----EAFRYADDVL-LEGVKG---VTDLI--VRPGL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 FLPTLKNKYDIFVSAPDLLGLDSVDGNEMVIKLLAHVKPGM 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 ILTYGYVSTPFRSEGPNRTRLANAGVKELAKY----VDTLIVV---PNQNLLALADKSTT 147
4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGL----GAGSKPELGKRSAEQQKVDIQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 8.4%; Score 74; DB 4; Length 327; I Similarity 27.7%; Pred. No. 2.2; 28; Conservative 20; Mismatches 33; Indels
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                                                                       29; Mismatches
                                                                                                                        DB 4; Length 1529;
                                                                       77; Indels
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APPLICANT: Guarent
APPLICANT: Austria
APPLICANT: Kennedy
                                                                                                                                                            Matches
                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08861464 Patent No. 5874210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/396,001
FILING DATE: 28-FEB-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09351
FILING DATE: 15-AUG-1994
PRIOR APPLICATION NUMBER: US 08/107,408
FILING DATE: 16-AUG-1993
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 781-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kennedy, Brian TITLE OF INVENTION: Genes TITLE OF INVENTION: in Yea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/861,464 FILING DATE: 22-MAY-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Mili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                             LENGTH:
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338 YYQWQGKKTSAQYYVNNAGVSVEDGCIWGTEGSGVGNW---APVVLGAGYTDGITYLSII 394
                                                                           278 SNTDINSLCVEGQGSAQAVNKVSGSIAICGTDYPGSENMVVPTVVGAGSSQPINVIKEDS 337
                                      47 -----GKRSAEQQKVDIQRMLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVV 101
                                                                                                                  12 ANTDCQAL-----GRSLAPHKIT-----LGKD-----ITKGLGAGSKPEL-----
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                                                                                                                                                                                                                                                                                                               450 amino acids
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Austriaco Jr., Nicanor
                                                                                                                                                          Conservative
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23.8%;
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                                                                                                                                                        20; Mismatches
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                                                                                                                                                                           Score 73.5;
Pred. No. 4
                                                                                                                                                                                             DB 2;
                                                                                                                                                          46;
                                                                                                                                                                                             Length 450;
                                                                                                                                                        Indels
                                                                                                                                                      33;
                                                                                                                                                      Gaps
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102 STPFRSEGPN 111

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SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-396-001-2
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                  Search completed: June 2, 2003, 08:47:47
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Job time : 28 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-396-001-2
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/396,001
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: MIT-6408A2
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-6240
TELEPHONE: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08396001 Patent No. 5919618
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guarente, Leonaro APPLICANT: Austriaco Jr., N. APPLICANT: Clus, James APPLICANT: Cole, Francesca APPLICANT: Kennedy, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genes Determining Cellular Senesence in TITLE OF INVENTION: Yeast NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA COUNTRY: US ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Mili
CITY: Lexington
STATE: MA
                                                                                    395 PNPNNKEAPN 404
                                                                                                                                102 STPFRSEGPN 111
                                                                                                                                                                           338 YYQWQGKKTSAQYYVNNAGVSVEDGCIWGTEGSGVGNW---APVVLGAGYTDGITYLSII 394
                                                                                                                                                                                                                                                              278 SNTDTNSLCVEGQGSAQAVNKVSGSIAICGTDYPGSENMVVPTVVGAGSSQPINVIKEDS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 PNPNNKEAPN 404
                                                                                                                                                                                                              47 -----GKRSAEQQKVDIQRMLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVV 101
                                                                                                                                                                                                                                                                                                       12 ANTDCQAL-----GRSLAPHKIT-----LGKD------ITKGLGAGSKPEL------ 46
                                                                                                                                                                                                                                                                                                                                                8.3%; Score 73.5; DB 2; Length 450; nilarity 23.8%; Pred. No. 4.1; Conservative 20; Mismatches 46; Indels 3
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Austriaco Jr., Nicanor
Claus, James
Cole, Francesca
                                                                                                                                                                                                                                                                                                                                                     46; Indels 33;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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               A_Geneseq_101002:*

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2: /SIDS2/gcgdata/g

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6: /SIDS2/gcgdata/g

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885
1 ASQLEGVEFIVANT
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Gapop 10.0 , Gapext 0.5
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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Pred. No. and is derived greater is the number of results predicted by chance to have ater than or equal to the score of the result being provided by analysis of the total score distribution. printed b

TI CON X AXX OX X COX X

18-OCT-2001. WO200177335-A2.

11-APR-2001; 2001WO-FR01118.

11-APR-2000; 2000FR-0004629.

(INSP ) INST PASTEUR.

No.	Score	Match Length DB	ength	89	ID	Description
ب	510	57.6	391	23	ABB48477	Listeria monocytog
N	495	55.9	410	22	AAU35046	Enterococcus faeca
ω	495	55.9	411	22	AAU33413	Enterococcus faeca
4	493	55.7	416	ພ	ABB55218	Lactococcus lactis
Ç	485	54.8	379	ນ	AAG81170	Mycobacterium tube
o,	480	54.2	390	21	AAY91108	Staphylococcus aur
7	480	54.2	390	21	AAY44710	S. pneumoniae mono
8	480	54.2	390	22	AAU34274	Staphylococcus aur
9	480	54.2	392	22	AAU37130	Staphylococcus aur
10	480	54.2	394	23	АВР39989	Staphylococcus epi

Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entlan K, Hauf J;

Maduenio E, De Rose M, Voss H;

4.5	44	ω.	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
285	304	323.5	37	424.5	429	433	435	435	435	435	439	440	441	441	447	447	447	447	447	452	452	452	452	456.5	463	463	464	464	466	470	472	472	472	472
32.2	34.4			æ	æ	8	9	٩	9	9	9	9	9	9		50.5	0	0	0	1	51.1	۲.	51.1	:	52.3	۲	۲.	52.4		ω.				
267	357	413	385	395	433	411	433	433	372	363	325	361	374	374	421	383	383	383	383	413	383	383	383	427	437	397	439	394	421	442	419	419	419	335
21	21	22	22	22	19	21	21	21	21	21	21	19	19	19	22	23	23	23	23	21	22	21	21	23	19	21	23	22	22	22	22	21	20	19
AAG04705	AAB01333	AAB96344	AAU35960	AAB96802	AAW41732	AAB01329	AAB01327	AAG46654	AAG46655	AAG46656	AAB01332	AAW51423	AAW41787	AAW70503	AAU35599	AAU76925	AAU76924	AAU76923	AAU76922	AAB01330	AAU34440	AAY91110	AAB15908	ABP25524	AAW41733	AAB01328	ABP25525	AAU36414	AAU60468	AAG92106	AAU37886	AAY44711	AAW99120	AAW80614
Arabidopsis thalia	Fts21 polypeptide	Ive P.	cter	~	idopsis chlo	0	уpе	thal	Arabidopsis thalia	Arabidopsis thalia	FtsZl polypeptide	Neisseria meningit	Brevibacterium fla	-	ï	N	. coli ftsz			<pre>21 polypept</pre>	-	cheric	E. coli proliferat	Streptococcus poly	Arabidopsis chloro	FtsZ2 polypeptide	Streptococcus poly	Pseudomonas aerugi	Propionibacterium		Streptococcus pneu	onomeric fila	reptococcus	S.pneumoniae filam

#### ALIGNMENTS

S	XX	X	X	××	DE	×	Ţ	×	AC	×	ID	ABB48477	RESU
Listeria monocytogenes.		vitamin B12; bacterial infection; disease.	Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;		Listeria monocytogenes protein #1181.		05-FEB-2002 (first entry)		ABB48477;		ABB48477 standard; Protein; 391 AA.	8477	RESULT 1

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RESULT 2
AAU35046
ID AAU3
XX AAU3
XX AAU3
XX AAU3
XX IS-F
AC Ente
XX Anti
XX Anti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L.
                                                                                                               21-MAR-2001;
                                                                                                                                                                                                                                                           Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
                                                                          21-MAR-2000;
                                                                                                                                                   27-SEP-2001.
                                                                                                                                                                                                                          Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                 Enterococcus faecalis cellular proliferation protein #333
                                                                                                                                                                                                                                                                                                                                                     13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              AAU35046 standard; Protein; 410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID No 1182; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQGVEFISVNTDAQALNIAKAETKLQIGTKLTRGLGAGAVPEIGKKAAEESREQIEEALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEAVDTLIVIPNDRLLQIVDKNTPMLEAFREADNVLRQGVQGISDLIAVPGLINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 AA;
                 2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                             2001WO-US09180
 2000US-253625P
                                                                          2000US-191078P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.6%; Score 510; DB 23; 56.0%; Pred. No. 1.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 3
AAU33413
ID AAU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the Greenes, their use in the discovery of novel antibiotics, the essential Greenes, their use in the discovery of novel antibiotics, the essential Greenes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella Greenemoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The Crimention is calso useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used Crimentify proteins used in proliferation, to express these proteins, Crimentify proteins used in proliferation, to express these proteins, Crimentify proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen crimentify of organisms. The present sequence represents an Crimential prokaryotic cellular proliferation protein.

Crimentification but was actually in the protein and control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                   WO200170955-A2
                                                                                                       Enterococcus faecalis
                                                                                                                                                                                   Antisense;
                                                                                                                                                                                                                                 Enterococcus faecalis cellular proliferation protein #49
                                                                                                                                                                                                                                                                                       14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                              AAU33413 standard; Protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                       antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
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16-FEB-2001; 2001US-269308P
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DB; AAS52905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GADMIFITAGMGGGTGTGAAPVVAKIAKELGALTVGVVTRPFSFEGPKRGRFAAEGIALL
                                                                                                                                                                             prokaryotic cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 495; DB 22;
Pred. No. 6.2e-44;
8; Mismatches 47;
                                                                                                                                                                                protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 410;
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ABB55218
ID ABB5
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                                                                                                                                                                                                                                                                                                                                                                                    CC prokaryotic cellular proliferation, their use in identifying the common and the encoded proteins. The prokaryotes used are CC genes, themselves and the encoded proteins. The prokaryotes used are CC Escherichia coil, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets correctly proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins used in proliferation, to express these proteins. CC The proteins used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery CC programmes. The artisense nucleic acid sequence is also useful to screen compounds in rational drug discovery CC avide variety of organisms. The present sequence is also useful to screen compounds in rational drug discovery CC avide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                       Matches 100;
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-2000;
23-MAY-2000;
26-MAY-2000;
               Lactococcus lactis protein ftsZ
                                                                  ABB55218;
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                         16-MAY-2002
                                                                                          ABB55218 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                ttp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                    2001-611495/70.
                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                          LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
                                                                                                                                                                                                                                                    VKGVEFITANTDVQALKHSKAETVIQLGPKYTRGLGAGSQPEVGQKAAEESEQVISESLQ
                                                                                                                                                   KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL
                                                                                                                                                                                                                                                                                                                                                         411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq ID No 4909; 511pp; English.
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen
Xu HH;
                                                                                        Protein; 416 AA
                                                                                                                                                                                                                                                                                                                  55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW,
                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                 Score 495; DB 22;
Pred. No. 6.3e-44;
                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                     47;
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                                                                                                                                                                                                                                                                                                                              Length 411;
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Best Local
13-NOV-2000; 2000WO-US31152
                          17-MAY-2001.
                                                 WO200135317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-043418/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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AAG81170 standard; Protein;
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Mycobacterium tuberculosis
                                                       Drug target; growth; organism viability; characterisation
                                                                                                               Mycobacterium tuberculosis potential drug target protein SEQ
                                                                                                                                                                                    04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequence useful in the identification or Lactococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GSDMIFITAGMGGGTGTGAAPVIAQIAKELGALTVGVVTRPFGFEGSKRSYFATEGIEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 VSGVEFIAANTDVQALRSSKADTVIQLGPKLTRGLGAGAQPEVGKRAAEESAETVSQALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANVDTLLIISNNNLLEIVDKKTPLTEALREADNVLRQGVQGVTDLITNPGMINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID No 1920; 2504pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                 379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 493; DB 2
Pred. No. 1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
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RESULT 6
AAY91108
ID AAY91108 standard; Protein; 390 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1999;
12-NOV-1999;
01-FEB-2000;
20-OCT-1999;
                                04-MAY-2000
                                                                 WO200024252-A1
                                                                                                    Staphylococcus aureus.
                                                                                                                                   microbial infection; screening.
                                                                                                                                                      Staphylococcus aureus; monomeric FtsZ; monomeric FtsA; antibacterial; Escherichia coli; multimeric protein; bacterial infection; vaccine;
                                                                                                                                                                                                                                               15-SEP-2000
                                                                                                                                                                                                         Staphylococcus aureus monomeric FtsZ protein sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                AAY91108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 172; 207pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH52021.
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                                                                                                                                                                                                                                                                                                                                                                                                       152 RESCDTLIVIPNDRLLQMGDAAVSLMDAFRSADEVLLNGVQGITDLITTPGLINV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 GADMVFVTAGEGGGTGGGAPVVASIARKLGALTVGVVTRPFSFEGKRRSNQAENGIAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKGVEFIAINTDAQALLMSDADVKLDVGRDSTRGLGAGADPEVGRKAAEDAKDEIEELLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                              (first entry)
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99US-0165124.
2000US-0179531.
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99WO-US24653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.8%; Score 485; DB 22; 54.3%; Pred. No. 6.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 7 AAY44710

AAY44710 standard; Protein; 390 AA

25-APR-2000 (first entry)

Monomeric filamentation temperature sensitive protein; FtsZ; dental treatment; vaccine; wound infection; gast

gastric ulcer;

S. pneumoniae monomeric filamentation temperature sensitive protein.

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19-APR-1999;
03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                       or inhibit the function of (I) selected from: (a) measuring the binding of a candidate compound to the polypeptide using a label; (b) measuring the binding of a candidate compound to (I) in the presence of a labeled competitor; (c) testing whether the candidate compound results in a signal generated by activation or inhibition of (I); or (d) detecting the effect of a candidate compound on the production of mRNA encoding (I) using e.g. enzyme linked immunosorbent assay (ELISA). AAY91108 to AAY91111 are useful as vaccines for treating microbial infections such as Staphylococcus, Streptococcus and Escherichia coli infections. The polypeptides are also useful for screening for antibacterial compounds and for detecting diseases associated with microbial infections. The present sequence represents Staphylococcus monomeric FtsZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated multimeric FtsZ:FtsA polypeptides (I) comprising the protein sequences given in AAY91108, AAY91110 and AAY91111. Also described are: (I) an antibody (Ab) specific for (I); (2) a method (M1) for treating an individual requiring enhanced or reduced activity or expression of (I) comprising administering an agonist or antagonist to (I), respectively; (3) a method (M2) for diagnosing a disease or susceptibility to a disease related to expression or activity of (I) comprising determining the presence or absence of a mutation in the nucleotide sequence encoding (I) and/or analysing for the presence or quantity of (I) in a sample; and (4) a method (M3) for screening to identify compounds that activate
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multimeric FtsZ:FtsA polypeptide, useful as a vaccine for treating bacterial infections and for diagnosing diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial infection
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                                                                                                                                                                                                                                                                                        Local
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155 KAAVDTLIVIPNDRLLDIVDKSTPMMEAFKEADNVLRQGVQGISDLIAVSGEVNL 209
                                           124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                        95
                                                                                                                                 64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                                                                                                                                                                   4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                        Similarity
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                                                                                    MNNVEFIAINTDGQALNLSKAESKIQIGEKLTRGLGAGANPEIGKKAAEESREQIEDAIQ
                                                                                                                                                                                                                                                                                                                                                       390 AA;
                                                                                                                                                                                                                                                                 Conservative
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99US-0129965.
99US-0132333.
                                                                                                                                                                                                                                                                                     54.2%; Score 480; DB 21; 54.3%; Pred. No. 2.3e-42;
                                                                                                                                                                                                                                                                 33; Mismatches
                                                                                                                                                                                                                                                                                                          DB 21;
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                                                                                                                                                                                                                                                                                                            Length 390;
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RRESULT 8
AAU34271
ID AAU3
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AC AAU3
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AC AAU3
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DT 14-F
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DT Stap
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KW Ant1
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PD 37-S
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Matches
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                                  WO200170955-A2
                                                                                                                                           Staphylococcus aureus cellular proliferation protein #550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide useful as a vaccine and for screening antimicrobial compounds for treating microbial diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal cancer; Helicobacter pylori infection; gastritis;
antibacterial; antiulcer; anti-inflammatory.
                                                                Staphylococcus aureus
                                                                                                antibiotic;
                                                                                                               Antisense;
                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                             AAU34274;
                                                                                                                                                                                                                                          AAU34274 standard; Protein; 390 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hensley CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200001801-A1
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                                                                                                                                                                                                                                                                                                                      155 KAAVDTLIVIPNDRLLDIVDKSTPMMEAFKEADNVLRQGVQGISDLIAVSGEVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Page 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                               35 MNNVEFIAINTDGQALNLSKAESKIQIGEKLTRGLGAGANPEIGKKAAEESREQIEDAIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    GADMVFVTSGMGGGTGTGAAPVVAKIAKEMGALTVGVVTRPFSFEGRKRQTQAAAGVEAM
                                                                                             prokaryotic cellular
; antibacterial; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 AA;
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                                                                                                                                                                           (first entry)
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                                                                                             lular proliferation protein;
drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 480; DB 21;
Pred. No. 2.3e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumonlae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
             Staphylococcus aureus cellular proliferation protein #1300
                                                                              AAU37130;
                                                                                                           AAU37130 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                           14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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N-PSDB; AAS52133.
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                      124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                  35 MNNVEFIAINTDGQALNLSKAESKIQIGEKLTRGLGAGANPEIGKKAAEESREQIEDAIQ
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 AA;
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                           392 AA
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Pred. No. 2.3e-42;
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RESULT 10
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                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
23-OCT-2000;
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23-MAY-2000;
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                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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                                                                                           95 GADMVFVTSGMGGGTGTGAAPVVAKIAKEMGALTVGVVTRPFSFEGRKRQTQAAAGVEAM
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                                                                                                         MNNVEFTAINTDGQALNLSKAESKIQIGEKLTRGLGAGANPEIGKKAAEESREQIEDAIQ
                                                                                                                                                                                                                                       392 AA;
                                                                                                                                                                                         Conservative
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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                                                                                                                                                                                       54.2%; Score 480; DB 22; 54.3%; Pred. No. 2.3e-42; tive 33; Mismatches 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW,
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
AAW80614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                     AAW80614 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                   MNNVEFIAINTDGQALNLSKAESKIQIGEKLTRGLGAGANPEIGKKAAEESREQIEDAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 AA;
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97US-064964P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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(first entry)

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RESULT 12
AAW99120
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                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AAV65301 to AAV65304) from the S. pneumoniae genome and corresponding protein sequences(AAW80605 to AAW80728). A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies that selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The antibodies can also be used to
                                 17-MAY-1999
                                                                                                AAW99120 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensitive, cell septation protein. The invention provides DNA sequences (AAV65201 to AAV65304) from the S. pneumoniae genome and corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a S. pneumoniae filamentous temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Pages 182-183; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detect S. pneumoniae cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-348529/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mills BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evaluating
                                                                                                                                                                                                          126 YVDTLIVVPNONLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                         38
                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                            HVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLRQGVQGITDLITNPGLINL 210
                                                                                                                                                                                                                                          DMVFITAGMGGGSGTGAAPVIARIAKDLGALTVGVVTRPFGFEGSKRGQFAVEGINQLRE 157
                                                                                                                                                                                                                                                                                                      GVEFIAANTDVQALSSTKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEETLTEAISGA 97
                                                                                                                                                                                                                                                                                                                                    GVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccus pneumoniae protein; recombinant; gene expression;
virulence; antibody; infection; detection; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norris FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                       335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgett SG,
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 filamentous temperature sensitive, cell septation protein.
pneumoniae ftsz protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression, and identification of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0036281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US22578
                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                      52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peery RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dehoff BS, Hoskins JA, Jaskunas
Peery RB, Rockey PK, Rosteck PR;
Solenberg PJ, Treadway PJ;
                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                               419 AA.
                                                                                                                                                                                                                                                                                                                                                                    Score 472; DB 19;
Pred. No. 1.3e-41;
5; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaskunas SR;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the infectious organism to drugs. FtsZ polypeptides and polynucleotides are also useful for screening for antagonists, agonists and drugs against infectious micro-organisms. FtsZ agonists and antagonists are bacteriostatic and bacteriocidal compounds which can be used in treatment to enhance (agonist) or block (antagonist or antisense sequence) ftsZ activity, therefore treating microbial diseases, especially Streptococcus pneumoniae diseases including otitis media, bacteraemia, conjunctivitis, pneumonia, sinusitis, pleural empyema, endocarditis and especially meningitis. Epitopes of ftsZ polypeptides and polynucleotides are useful immunogens for producing anti-ftsZ antibodies for prevention of bacterial infections, and ftsZ polynucleotions can be used in genetic immunisation (gene therapy) to prevent infections. FtsZ polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful ruse on wounds and body implants to prevent actions infections and are useful constituted and constitute the prevent actions and body implants to prevent actions and sequence of the constitutions and sequence of the constitutions and constitutions are useful constitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is ftsZ polypeptide isolated from Streptococcus pneumoniae. FtsZ polypucleotides and polypeptides are useful for diagnosing susceptibility of diseases by detecting mutations or polymorphisms in the ftsZ gene or analysing for the presence of amount ftsZ polypeptide expressed in a patient sample. FtsZ PCR probes are useful for diagnosing diseases, and can characterise the response of the probability of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, and are useful for use on wounds and body implants to prevent bacterial infection. FtsZ polypeptides and polynucleotides may also be used as reagents for differential screening methods e.g. using ftsZ probes in RT-PCR to identify and quantify genes expressed in bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus pneumoniae ftsZ polypeptide and polynucleotide useful as diagnostic reagents and for prevention and treatment of Streptococci infections which cause bacteraemia, otitis media and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 4; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae; fts2; antibacterial; microbial disease; otitis media; bacteraemia; conjunctivitis; pneumonia; sinusitis; pleural empyema; endocarditis; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX19269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fueyo JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP899334-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
    126 YVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                            38
                                                                                                                                                                                                                                                                                                                                                                                                 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                            NMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKELAK 125
                                                                                                                                                                                                                                                                                                                 GVEFTVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDS 65
                                                                                    DMVFITAGMGGGSGTGAAPVIARIAKDLGALTVGVVTRPFGFEGSKRGQFAVEGINQLRE
                                                                                                                                                                                                                                        GVEFIAANTDVQALSSTKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEETLTEAISGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0055720.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     53.3%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 472; DB 20;
Pred. No. 1.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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HVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLRQGVQGITDLITNPGLINL

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RESULT 14
AAU37886
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                       temperature sensitive protein (FtsZ). This is related by amino acid sequence homology to Lactococcus lactis FtsZ AAU74322. Multimeric FtsZ protein is useful in identifying compounds that modulate its function. The protein and its variants are useful in diagnosing and treating microbial diseases and for prophylactic use in dental treatment. They can be used as vaccines to prevent wound infections by bacteria especially S. pneumoniae. Agonists and antagonists are useful in treating diseases caused by Helicobacter pulpori infections e.g.
             AAU37886 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 4; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide useful as a vaccine and for screening antimicrobial compounds for treating microbial diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monomeric filamentation temperature sensitive protein.
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                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 gastroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the monomeric filamentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hensley CP, Pearce KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; antiulcer; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal cancer; Helicobacter pylori infection; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FtsZ; dental treatment; vaccine; wound infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monomeric filamentation temperature sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                              isolated from Streptococcus pneumoniae or Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-171008/15.
                                                                                            158 HVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLRQGVQGITDLITNPGLINL 210
                                                                                                                         126 YVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                       98 DMVFITAGMGGGSGTGAAPVIARIAKDLGALTVGVVTRPFGFEGSKRGQFAVEGINQLRE
                                                                                                                                                                                        66
                                                                                                                                                                                                                     38 GVEFIAANTDVQALSSTKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEETLTEAISGA
                                                                                                                                                                                                                                                                                                                                                                                             ointestinal cancer, gastric ulcer and gastritis.
The specification is unclear as to whether this sequence was
                                                                                                                                                                                                                                                                                     91;
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                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ49959
                                                                                                                                                                       NMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKELAK
                                                                                                                                                                                                                                                   GVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDS
                                                                                                                                                                                                                                                                                                                                                  419 AA;
                                                                                                                                                                                                                                                                                    Conservative
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             Protein; 419
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                                                                                                                                                                                                                                                                                                    53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sossong TM;
                                                                                                                                                                                                                                                                                    35;
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                                                                                                                                                                                                                                                                                                 Score 472; DB 21;
Pred. No. 1.8e-41;
                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                Length 419;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastric ulcer;
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                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                              Query Match
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23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                            to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                        prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic cellular proliferation protein, antibiotic; antibacterial; drug design.
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000;
23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae cellular proliferation protein #315.
                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200170955-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                Local
 98
                  66 NMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKELAK 125
                                                                38 GVEFIAANTDVQALSSTKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEETLTEAISGA
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                                                                                                                                 91;
                                                                                                                                                Similarity
 DMVFITAGMGGGSGTGAAPVIARIAKDLGALTVGVVTRPFGFEGSKRGQFAVEGINQLRE
                                                                                   GVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq ID No 13479;
                                                                                                                                                                                                419 AA;
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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2000US-206848P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu HH;
                                                                                                                                                53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW,
                                                                                                                                 35;
                                                                                                                                                Score 472; DB 22; Pred. No. 1.8e-41;
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                                                                                                                               Mismatches
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                                                                                                                                                              Length 419;
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YVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178

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RESULT 15
AAG92106
ID AAG92
XX AAG92
XX 26-SE
XX 26-SE
XX Coryn
KW Coryn
XX Coryn
XX Coryn
XX Coryn
XX 16-DE
PR 16-DE
XX INAKAG
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XX WPI;
DR WPI;
DR N-PSD
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                                                                                                                                                                                                                                                                                                           Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium. and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; SEQ ID NO: 5860; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000EP-0127688.
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124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
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                                                        92;
                                                                                                                                                                                                                                                                                                  h 53.1%; Score 470; DB 22; Length 442;
Similarity 52.6%; Pred. No. 3.1e-41;
92; Conservative 36; Mismatches 47; Indels
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Senoh A, Ikeda M, Ozaki A;
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Search completed: June 2, 2003, 08:33:21 Job time: 72 secs

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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
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 Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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seq length: 0 seq length: 2000000000
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Match
 is the number of results predicted by chance to have ter than or equal to the score of the result being pr
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(without alignments)
77.330 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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3: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
0: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                      Length DB
Match
                                                                 US-09-770-509-2
US-09-770-509-17
US-09-770-509-15
US-09-770-509-15
US-09-770-509-13
US-09-770-509-16
US-09-15-242-4009
US-09-770-509-16
US-09-770-509-11
US-09-770-509-10
US-09-770-509-11
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                  Sequence 2, Appli
Sequence 11, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 16639, Appl
Sequence 211, Appl
Sequence 211, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 17723, Appl
Sequence 12723, Appl
Sequence 12723, Appl
Sequence 12, Appl
Sequence 13479, Appl
Sequence 13479, Appl
                                                                                                                                                                                                                                                                   Description
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### ALIGNMENTS

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Sequence 2, Application US/09770509

Publication No. US20030082657A1

GENERAL INFORMATION:
APPLICANT: KAtagiri, F.
TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR
TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES
FILE REFERENCE: NADII 018A
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Phytophthora infestans
US-09-770-509-2
                   RESULT 2
US-09-770-509-17
; Sequence 17, Application US/09770509
; Publication No. US20030082657A1
; GENERAL INFORMATION:
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US-09-770-509-2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 178;
APPLICANT: Katagiri, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                         1 ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR 60
                                                                                                                                                               KELAKYVDTLIVVPNQNLIALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                  MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
                                                                                                                                                                                                                                                                                                                                   ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR 60
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US-09-738-626-5860 US-09-770-509-25 US-09-770-509-26

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RESULT 4
US-09-770-509-15
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US-09-770-509-14
Sequence 14, Application US/09770509
Publication No. US20030082657A1
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                                   GENERAL INFORMATION:
                                                       Sequence 15, Application US/09770509 Publication No. US20030082657A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 14
LENGTH: 452
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CURRENT FILTNG DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENCTH: 401
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Katagiri, F.
TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR
TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES
TITLE OF INVENTION: COMYCETE FTSZ-MT AS
                   APPLICANT: Katagiri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: NADII.018A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                             156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 RSLEDRYDTLIIIPNQNIFKLINASTSMADAFGLADDILLAGVKSITDLMYRPGLINL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 YIADANMVFITAGMGGGTGTGAAPVVAEVCMEKDILTVAVVTKPFSFEGKHRARLANEGI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 ARKLSGVEFVCANTDAQHLSTCLTENKLQLGKESTQGLGCGANPESGRRAAEESKEEIAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR 60
                                                                                                                                                                                                                                                                                LQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVK 121
                                                                                                                                                                       ELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                              LENSNMYFITAGMGGGTGTGSAPIIARIAKELGILTVGVVTKPFHFEGGHRMKTADKGLI 155
                                                                                                                                                                                                                                                                                                                        ANLQGANFVVANTDAQSLEHSLCINKIQLGVSTTRGLGAGASPEVGALAAQESENEIRSS 95
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      58.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.5%; Score 527; DB 9; Length 401; 58.4%; Pred. No. 4.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 518; DB 9;
Pred. No. 4.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
A TARGET FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 452;
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                                                                                                                        US-09-815-242-10639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bartonella clarridgeiae
US-09-770-509-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-770-509-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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; TYPE: PRT
; ORGANIZM: Caulobacter crescentus
US-09-770-509-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 13
LENGTH: 581
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09770509
Publication No. US20030082657A1
GENERAL INFORMATION:
APPLICANT: Katagiri, F.
TITLE OF INVENTION: OMNICETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: AMTIMICROBIAL-SPECIFIC BIOCIDES
FILE REFERENCE: NADII.018A
                                                             GENERAL INFORMATION:
                                                                                   Sequence 10639, Application Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES FILE REPERENCE: NADII 018A CURRENT EFFECTION NUMBER: US/09/770,509 CURRENT FILING DATE: 2001-01-25 NUMBER OF SEQ ID NOS: 32 SOFTMARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 5/...
nes 101; Conservative
                                                                                                                                                                                                             158 QKSVDTLIVIPNQNLFRIANEKTTFSDAFAMADQVLYSGVASITDLMIKEGLINL
                                                                                                                                                                                                                                                     124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102;
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                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                      64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                  38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 GAHMVFITAGMGGGTGTGAAPIIAKCARERGILTVGVVTKPFHFEGRHRMRLADSGIQEL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 LEGVEFVVANTDAQQLQFAKTDRRIQLGVQITQGLGAGAHPEVGMSAAEESFPEIGEHLD 97
                                                                                                                                                                                                                                                                                                                                                                                                                         4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
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                                                                                                                                                                                                                                                                                                 DSHMVFITAGMGGGTGTGAAPVVANAAREKGILTVGVVTKPFQFEGARRMKTAEAGIEEL
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.0%; score 496; DB 9; Length 581; 57.7%; Pred. No. 1.4e-43;
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                                                                                                         US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Ge;
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J.
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 14110
SOFTWARE: FASTSEO for Windows Version 4.0
SEO ID NO 10639
LENCTH: 410
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.9%; Score 495; DB 10; Best Local Similarity 57.1%; Pred. No. 1.1e-43; Matches 100; Conservative 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
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US-09-770-509-16

; Sequence 16, Application US/09770509
; Publication No. US20030082657A1
; GENERAL INFORMATION:
; APPLICANT: Katagiri, F.
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; OTHER INFORMATION: Xaa - Any Amino Acid
US-09-815-242-4909
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 16
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LENGTH: 411
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                                                                                                                                                                                                                                                                                                Query Match
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Best Local (
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CURRENT FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BICCIDES FILE REFERENCE: NADII.018A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Cyanidioschyzon merolae
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 407
                                                                                                                                                                                                                                                                            Local Similarity
                      121 KELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
237 VELTEHVDTMLVIPNQNLFKVASPRTSFLDAFRLADHVLYSGVRSITDLMTVPGLINL 294
                                                                                177 EFRGYHLLFYTAGMGGGTGTGAAPIIARAAAELGCLTVAVVTKPFHFEGMIRMKTAEQGI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100;
                                                                                                                          61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
                                                                                                                                                                                                                                                        95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 VKGVEFITANTDVQALKHSKAETVIQLGPKYTRGLGAGSQPEVGQKAAEESEQVISESLQ
                                                                                                                                                                                          1 ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.9%;
Similarity 57.1%;
                                                                                                                                                                    ASSLPGVEFLVANTDAQALKMSLCPNRIQLGASLTEGLGAGARPDIGRAAAEEAYETLKR 176
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for Windows Version 4.0
                                                                                                                                                                                                                                                                          55.4%; Score 490; DB 9; 53.4%; Pred. No. 3.6e-43;
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Pred. No. 1.1e-43;
                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                        49;
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RESULT 10
US-09-770-509-11
Sequence 11, Application US/09770509
Publication No. US20030082657A1
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US-09-712-363-221
                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Katagiri,
                                                SEQ ID NO 11
LENGTH: 583
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Best Local S
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                                                                                          TITLE OF INVENTION: COMYCETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BICCIDES EILE REFERENCE: NADII.018A

CURRENT APPLICATION NUMBER: US/09/770,509

CURRENT FILING DATE: 201-01-25

NUMBER OF SEO ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/134,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-03-26
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PRIOR APPLICATION NUMBER: 60/126,593
ORGANISM: Agrobacterium
                               TYPE: PRT
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FILLING DATE: 1999-11-12
APPLICATION NUMBER: 60/165,086
FILLING DATE: 1999-11-12
R OF SEQ ID NOS: 292
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54.3%; Pred. No. 1.1e-42;
75. Mismatches 45;
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BY COMPARATIVE ANALYSIS
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US-09-770-509-10
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                                                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                 Sequence 5770, Application US/09815242 Patent No. US20020061569A1
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                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Katagiri, F.
TITLE OF INVENTION: OMMYCETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES FILE REFERENCE: NADII.018A
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                          TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 RVQGANMMFVTAGMGGGTGTGAAPVIAQAALDAGILTVAVVTKPFRFEGNNRAKLAAQGL 248
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                                                                                                            Xu, H. Howard
                                                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                                                                                 Yamamoto, Robert T.
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51.7%;
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Pred. No. 3.3e-42;
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                                                                                       of Essential Genes
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
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: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 5770
: LENGTH: 390
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-09-815-242-5770
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER CE CONTROL DATE: 2001-02-16
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant J.
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RESULT 15
US-09-754-608-2
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APPLICANT: Fuery, Joanna Lynn
APPLICANT: Lonetto, Michael A.
APPLICANT: Lonetto, Michael A.
APPLICANT: Pearce, Kenneth
TITLE OF INVENTION: ftsz
FILE REFERENCE: GM10068
CURRENT APPLICATION NUMBER: US/09/754,608
CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 09/120,426
PRIOR APPLICATION NUMBER: 1998-07-22
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; LENGTH: 392
; TYPE: PRT
; ORCANISM: Staphylococcus aureus
US-09-815-242-12723
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APPLICANT: KATAGIRI, F.

TITLE OF INVENTION: OMMYCETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES FILE REFERENCE: NADII.018A
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                     Sequence 2, Application US/09754608 Patent No. US20020004580A1
                                                                                                                                                                                GENERAL INFORMATION:
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Publication No.
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Best Local
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TYPE: PRT
ORGANISM: Sinorhizobium meliloti
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Local Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                    124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                     158 QKSYDTLIVIPNQNLFRIANDKTTFADAFAMADQVLYSGVACITDLMVKEGLINL 212
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                                                                                                                                                                                                                                                                                                                                                                                                 98 GTHMCFVTAGMGGGTGTGAAPIVAQAARNKGILTVGVVTKPFHFEGGRRMRIADQGISDL
                                                                                                                                                                                                                                                                                                                                                                                                                    64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILIVGVVSTPFRSEGPNRTRLANAGVKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Pred. No. 2.2e-41;
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Pred. No. 3.8e-42;
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PRIOR APPLICATION NUMBER: 60/055,720

PRIOR FILING DATE: 1997-08-12

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

EARLY 1997

OUGHTH: 419

OUGHTH: 419
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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885
1 ASQLEGVEFIVANT
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1: /cgn2_6/ptodata/1/paa//

2: /cgn2_6/ptodata/1/paa//

3: /cgn2_6/ptodata/1/paa//

4: /cgn2_6/ptodata/1/paa//
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                                                     ASQLEGVEFIVANTDCQALG.....LLEGVKGVTDLIVRPGLINL 178
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                               /cgn2_6/ptodata/1/paa/US60_COMB.pep:*
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## SUMMARIES

6 51	5 527 5 520	3 52	2 5		No. Score	Result	
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452	401 370	401	336	178	Match Length DB ID		
	21 US-09-791-537-130384 21 US-09-791-537-1723		21 US-09-791-537-32478	100.0 178 21 US-09-770-509-2	8 ID		
Sequence 14, Appl	Sequence 130384,	Sequence 17, Appl	Sequence 32478 A	Sequence 2, Appli	Description		

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#### ALIGNMENTS

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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Phytophthora infestans
US-09-770-509-2
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09770509
GENERAL INFORMATION:
APPLICANT: Katagiri, F.
TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR
TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES
FILE REFERENCE: NADII.018A
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Best Local s
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                       61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
                                                                          h 100.0%; Score 885; DB 21; Similarity 100.0%; Pred. No. 6.4e-91; 78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    Length 178;
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RESULT 3
US-09-770-509-17
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; LENGTH: PRT
; ORGANISM: Mallomonas splendens
US-09-770-509-17
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US-09-791-537-32478
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US-09-791-537-32478
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GENERAL INFORMATION:
APPLICANT: Katagiri, F.
TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR
TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES
FILE REFERENCE: NADII.018A
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APPLICANT: Bionomix, Inc.
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LENGTH: 336
TYPE: PRT
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
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APPLICANT:
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                      160 YIADANMVFITAGMGGGTGTGAAPVVAEVCMEKDILTVAVVTKPFSFEGKHRARLANEGI
                                                                                                              100 ARKLSGVEFVCANTDAQHLSTCLTENKLQLGKESTQGLGCGANPESGRRAAEESKEEIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 EELQKHVDTLIVIPNQNLFLIANPNTTFKQAFQMADEVLQQGVRGITDLMVCPGLINL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 ALEGARMCFIAAGMGGGTGTGAAPVIAKVARDRGILTVGVVTKPFNFEGKRRARSAESGI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
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                                                                61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
                                                                                                                                                     1 ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR 60
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                                                                                                                                                                                              59.5%; Score 527; DB 21; 58.4%; Pred. No. 5.8e-50; tive 27; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                          Length 401;
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                                                                                                                                                                                                Gaps
                                                                                                              159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: HHEEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1723, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 130384
                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1723
                                                                                                                                                                              Matches 103;
                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                 LENGTH: 370
TYPE: PRT
ORGANISM: Clostridium lentocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 59.5%; Score 527; DB 21; Local Similarity 58.4%; Pred. No. 5.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 YIADANMVFITAGMGGGTGTGAAPVVAEVCMEKDILTVAVVTKPFSFEGKHRARLANEGI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ARKLSGVEFVCANTDAQHLSTCLTENKLQLGKESTQGLGCGANPESGRRAAEESKEEIAR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 RSLEDRVDTLIIIPNQNIFKLINASTSMADAFGLADDILLAGVKSITDLMVRPGLINL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KELAKYYDTLIVVPNQNLLALADKSTIMLEAFRYADDVLLEGVKGYTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 RSLEDRVDTLIIIPNQNIFKLINASTSMADAFGLADDILLAGVKSITDLMVRPGLINL 277
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    95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR 60
                                                                                                                                  4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
Conservative
                                                                                                                                                                              Conservative
                                                                                                                                                                                                58.8%; Score 520; DB 21; 58.9%; Pred. No. 3.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; Mismatches
                                                                                                                                                                              30; Mismatches
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                                                                                                                                                                                                                       Length 370;
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Sequence 14, Application US/09770509
GENERAL INFORMATION:
APPLICANT: KATAGITI, F.
TITLE OF INVENTION: COMYCETE FTSZ-MT AS A TARGET FOR
TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES
FILE REFERENCE: NADII.018A
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
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US-09-791-537-69060
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US-09-770-509-14
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261,/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 69060
LENGTH: 452
                                                                                                                                                                       Matches
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                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                          Query Match
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Local Similarity 55.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 ANLQGANFVVANTDAQSLEHSLCINKIQLGVSTTRGLGAGASPEVGALAAQESENEIRSS 95
                                                                                                                           2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM 61
                                                                                                                                                                       99;
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09791537
                                                                                                                                                                                58.5%; Score 518; DB 21; 55.9%; Pred. No. 7.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Mismatches 40;
                                                                                                                                                                   38; Mismatches
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US-09-791-537-40338
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; TYPE: PRT
; ORGANISM: Wolbachia
US-09-791-537-40309
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 40338
LENGTH: 289
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APPLICANT: Dobe, Derek
APPLICANT: Dobe, Derek
APPLICANT: Doseph
APPLICANT: Doseph
TITLE OF INVENTION: THEE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 40309
                                                                 Matches 107;
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40338, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                      Match 58.2%;
Local Similarity 56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 MVMPGLINL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 VRRMRIAELGLEELQKYVDTLIVIPNQNLFRIANEKTTFSDAFKLADNVLHIGIRGVTDL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 IVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 PNRTRLANAGVKELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 IKDSHMLFITAGMGGGTGTGAAPVIAKAAREARAAVKDRAPKEKKILTVGVVTKPFGFEG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LQDSNMLFITGGMGGGTCTGAAPVVASVAREL-------GILTVGVVSTPFRSEG 109
2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNLQGVNFVVANTDAQALEKSLCDKKIQLGINLTKGLGAGALPDVGKGAAEESIDEIMEH 61
                                                                 Conservative
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                                                          28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                            Score 515; DB 21,
Pred. No. 8e-49;
Pred. No. 8e-49; Indels
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                                                                                                   DB_21; Length 289;
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                                                              12;
                                                          Gaps
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2 SNLQGVNFIVANTDAQALEKSLCDKKIQLGINLTKGLGAGALPDIGKGAAEESIDEIMEH 61

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; TYPE: PRT
; ORGANISM: Wolbachia
US-09-791-537-40306
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US-09-791-537-40306
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APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 40306
                                                        APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 40308
TENET: DEBE
                                                                                                                                                                                                                                                                                                                                                             Sequence 40308, Application US/09791537 GENERAL INFORMATION:
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ORGANISM: Wolbachia sp
                                             TYPE: PRT
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US-09-791-537-29481 ; Sequence 29481, Application US/09791537
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US-09-791-537-40312
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APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 40312
LENGTH: 289
TYPE: PRT
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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Similarity 56.1%; Pred. No. 1e-48;
06; Conservative 29; Mismatches 42; Indels 1
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RESULT 15
US-09-791-537-132641
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; Sequence 105171, Application US/09791537

; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 29481
LENGTH: 398
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US-09-791-537-29481
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APPLICANT: Dabe, Derek
APPLICANT: Derek
APPLICATION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 105171
LENGTH: 399
TWORE: Dame
Sequence 132641, Application US/09791537 GENERAL INFORMATION:
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Best Local Similarity
Matches 101; Conserva
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Best Local S
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                                                                                                                    170 IVRPGLINL 178
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Search completed: June Job time: 276 secs
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US-09-791-537-132641
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Matches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 132641
LENGTH: 399
TYPE: PRT
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APPLICANT: Danzer, JOseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                                                                                                                                                                                                                     Local Similarity
wes 101; Conserv
                                                                                                                                             47 VEFIVANTDLQALQTSIAPIKIALGAKVTAGLGAGGKPEIGQAAAEEDIDVIRNHLSGAD
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                                                                          VDTLIIIPNQKLLTVVDKRTTIKDAFKRADDVLRMGVQGIAGLIIEHGEVNI 218
                                                                                                                                                                                                                                                                                                   57.2%; Score 506; DB 21; llarity 58.7%; Pred. No. 1.3e-47; Conservative 27; Mismatches 44;
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Sequence 42973	Sequence 17767	Sequence 76027	Sequence 75194	Sequence 44660	Sequence 72045	Sequence 6, App	Sequence 77931	Sequence 74650	Sequence 24128	Sequence 24128	Sequence 66647	Sequence 76497	Sequence 63205	Sequence 21663	Sequence 21663	Sequence 21663	Sequence 69702	Sequence 67907
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ALIGNMENTS

#### APPLICANT: Travick, John APPLICANT: Carr, Grant APPLICANT: Yamamoto, Robert APPLICANT: Yamamoto, Robert APPLICANT: Forsyth, R: APPLICANT: Forsyth, R: APPLICANT: Travick, John FIILE REFERENCE: ELITER.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/230,335 PRIOR APPLICATION NUMBER: 60/230,335 PRIOR APPLICATION NUMBER: 60/230,347 PRIOR FILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: 60/242,578 PRIOR APPLICATION NUMBER: 60/242,578 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR APPLICATION NUMBER: 60/257,931 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16 RESULT 1 US-10-282-122A-60624 SOFTWARE: Pate SEQ ID NO 60624 LENGTH: 391 Sequence 60624, App. GENERAL INFORMATION APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614 APPLICANT: Wang, ORGANISM: Listeria monocytogenes PatentIn version Ohlsen, Kari Zyskind, Judith Zamudio, Carlo Malone, Cheryl Haselbeck, Robert Application US/10282122A Liangsu Daniel Carlos See File Wrapper or in Microorganisms

US-10-282-122A-60624

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SEQ ID NO 51618
LENGTH: 373
                                                                                                                  Query Match
                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-11-
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                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/230,347
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                                                                                                Similarity
LKNVEFTAINTDKQALALSQASQKIQIGDKLTKGLGAGANPEIGQKAAEESKDEISQAIK 94
                LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
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Malone, Cheryl
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Forsyth, R.
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                                                                              Conservative
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                                                                                          57.3%; Score 507; DB 6; 56.0%; Pred. No. 3.9e-39;
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US-10-282-122A-47081
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LENGTH: 404
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                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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GENERAL INFORMATION
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/242,578
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                     127 VDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                      112 MVFITAGMGGGTGTGAAPVIAQVAKELGILTVGVVTKPFKFEGPKKLRLAEQGINNLRKS
                                                                                                                  67 MLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKELAKY 126
                                                                                                                                                              52 VEFTVANTDLQALQTSTAPIKTALGAKVTAGLGAGGKPETGQAAAEEDIDVIRNHLSGAD
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                                                                                                                                                                                         7 VEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDSN 66
                                                                                                                                                                                                                                                                                   Similarity
Carr, Grant
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Malone, Chery
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                57.2%; Score 506; DB 6; 58.7%; Pred. No. 5.5e-39;
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 45663
LENGTH: 386
TYPE: PRT
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GENERAL INFORMAT
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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FILING DATE: 2000-12-2
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
155 KENVDTLIVIPNDRLLEIVDKNTPMLEAFREADNVLRQGVQGISDLIATPGLINL 209
                                   124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
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                                                                                                          64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                  Carr, Grant
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Malone, Cheryl
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US-10-282-122A-53331
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Sequence 53331, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                Similarity
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Zyskind, Judith
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Malone, Cheryl
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Haselbeck, Robert

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; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53331
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US-10-282-122A-42469
; Sequence 42469, Application US/10282122A
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                               102 LQGADMVFVTAGMGGGTGTGAAPVVAGLAKEMGILTVGVVTKPFAFEGKIRMKNAEGGIA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 AQLKGVEFISVNTDKQALYTSKAEYKVQIGEKLTRGLGAGANPEVGKRAAEESKDEIVKL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                       ELKSKYDTLITIPNDRLLQIYQKNTSMLDAFAYADDYLKQGIQSISDLIAVEGLINL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wall, Danies
                                                         Wall, Daniel
                                                                                   Ohlsen, Kari
Zyskind, Judith
                                                                                                                                               Zamudio, Carlo
Malone, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
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                  Carr, Grant
                                       Trawick, John
                                                                                                                              Haselbeck, Robert
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                                                                                                                                                                                               Liangsu
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                                                                                                                                                                          Carlos
Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; score 505; DB 6; Length 394; 55.9%; Pred. No. 6.5e-39;
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RESULT 8
US-09-134-000C-4658
US-09-134-000C-4658, Application US/09134000C
Sequence 4658, Application US/09134000C
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                                                  US-09-134-000C-4658
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                                                                                                                                                SEQ ID NO 4658
Query Match
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                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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PRIOR FILING DATE: 2000-05-23
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CURRENT APPLICATION NUMBER: US/10/282,122A
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                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4
TYPE: PRT
                                                                            ORGANISM: Enterococcus faecalis
                                                                                                                       LENGTH: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 KENYDTLLIISNNRLLEVYDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AKYYDTLIYVPNQNLLALADKSTTMLEAFRYADDVLLEGYKGYTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 GADMIFITAGMGGGTGTGAAPVVAKIAKELGALTVGVVTRPFSFEGPKRGRFAAEGIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 VKGVEFITANTDVQALKHSKAETVIQLGPKYTRGLGAGSQPEVGQKAAEESEQVISESLQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.9%; Score 495; DE 57.1%; Pred. No. 6e-3 tive 28; Mismatches
  55.9%;
     Score 495;
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  Length 435;
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US-09-134-000C-4658
US-09-134-000C-4658, Application US/09134000C
GENERAL INFORMATION:
GENERAL TOWNSHIP OF THE PROPERTY OF THE PROPER
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APPLICANT: Zamudd
APPLICANT: Malone
APPLICANT: Haselt
APPLICANT: Ohlser
APPLICANT: Zyskit
APPLICANT: Wall,
APPLICANT: Wall,
APPLICANT: Trawic
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13
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Trawick, John
                                                                                                                                                                                                                     Yamamoto,
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Zyskind, Judith
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Malone, Cheryl
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                                                                                                                                                                                                                         Robert
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                                                                                                      Microorganisms
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                                                                                                                                                                                                                                                                                                Sequence 7295, Application US/10417884
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn SEQ ID NO 57592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/267,636
PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR
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TYPE: PRT
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_FEATURE
LOCATION: (343)...(343)
OTHER INFORMATION: X-any amino acid
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               SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/10/417,884
                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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APPLICATION NUMBER:
FILING DATE: 2000-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 VKGVEFITANTDVQALKNSKAETVIQLGPKYTRGLGAGSQPEVGQKAAEESEQSLREALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.8%; Score 494; DB 6; 1 Similarity 55.4%; Pred. No. 7.5e-38; 97; Conservative 31: Microsite 1
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                                                                     OPERATING SYSTEM: <Unknown>
                                                                                              COMPUTER: PC
                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                               STREET:
FILING DATE: 17-Apr-2003
                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         version
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                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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RESULT 12
US-10-282-122A-61968
: Sequence 61968, Application US/10282122A
: GENERAL INFORMATION:
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Best Local S
Matches 97
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23 PRIOR PRIOR DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/203,335
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APPLICANT:
APPLICANT:
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APPLICANT: Zamuc
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ. ID NO: 7295:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 7295:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GADMIFITAGMGGGTGTGAAPIVAGIAKELGALTVGVVTRPFTFEGPKRGRFAAEGIARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 VKGVEFITANTDVQALKNSKAETVIQLGPKYTRGLGAGSQPEVGQKAAEESEQSLREALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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Zyskind, Judith
                                                                                                                                                                                                                                                                                  Carr, Grant
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Malone, Cheryl
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(B) LOCATION 1...414
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SOFTWARE: Patentin version 3.1
                                                                                             PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITA. 034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                        APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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                                        APPLICATION NUMBER:
APPLICATION NUMBER:
                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 RESCDTLIVIPNDRLLQMGDAAVSLMDAFRSADEVLLNGVQGITDLITTPGLINV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 GADMYFYTAGEGGGTGTGGAPVVASIARKLGALTVGVVTRPFSFEGKRRSNQAEAGINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 LKGVEFIAINTDAQALLMSDADVKLDVGRDSTRGLGAGADPEVGRKAAEDAKDEIEELLR
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Malone, Cheryl
Haselbeck, Robert
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                                                                                                                                  NUMBER: 60/207,727
2000-05-26
                    2000-10-23
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                                      60/242,578
                                                                                                                   60/230,335
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PCT-US02-36122-84

Sequence 84, Application PC/TUS0236122

; GENERAL INFORMATION:
APPLICANT: Murphy, Ellen and Projan, Stephen, j.
APPLICANT: MUrphy, Ellen and Projan, Stephen, j.
FIILE OF INVENTION: Alloiococcus otitidis Infectious Disease Targets
FILE REFERENCE: Application 1
; CURRENT APPLICATION NUMBER: PCT/US02/36122
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 84
; LENGTH: 410
TYPE: PRT
                                                                           PCT-US02-36123-5202
FCT-US02-36123-5202
Sequence 5202, Application PC/TUS0236123
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Allolococcus otitidis PCT-US02-36122-84
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 52722
LENGTH: 369
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Best Local Similarity
APPLICANT: American Cyanamid Company, and Fletcher, Leah D., McMichael, John C., APPLICANT: Russell, David P., and Zagursky, Robert J. TITLE OF INVENTION: Alloiococcus otitidis Open Reading Frames (ORFs) Encoding Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Госат
                                                                                                                                                                                                                                          155 KERYDTLYTIPNERLLSIVDKKTSLMDSFKLADDYLRQGYQGISDLITIPGLYNL 209
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PCT-US02-36123-5202
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antigens, Immunogenic Compositions and Uses Thereof FILE REFERENCE: Application 1
CURRENT APPLICATION NUMBER: PCT/US02/36123
CURRENT FILING DATE: 2003-01-02
NUMBER OF SEQ ID NOS: 6653
SOFTWARE: Patentin version 3.1
SEQ ID NO 5202
LENGTH: 410
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Title: Perfect score: US-09-770-509-2 885 1 ASQLEGVEFIVANT

Sequence: ASQLEGVEFIVANTDCQALG.....LLEGVKGVTDLIVRPGLINL 178

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

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pir1:*
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Database :

PIR_73:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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cell division prot	cell division prot	cell division prot	cell division prot	plastid division p	plastid division p	chloroplast divisi	plastid division p		cell division prot	probable cell divi

### ALIGNMENTS

Cell division protein ftsz [imported] - Rickettsia conorii (strain Malish 7) C;Species: Rickettsia conorii and Rickettsia prowazekii C;Accession: 697826 R;Qoata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Goata H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, D.; R;Rcleuie; Tele: Audic, S; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R;Rcleuie; Tele: Audic, S; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R;Rcleuie; Tele: Audic, S; Renesto-Audiffren, P.; Fournier, P. E; Barbe, V.; Samson, D.; R;Rcleuie; Tele: Audic, S; Renesto-Audiffren, P.; Fournier, P. E; Barbe, V.; Samson, D.; R;Rcleuie; Tele: Audic, P. Renesto-Audiffren, P.; Alsmark A;Residues; Tele: Audic, P.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark A;Residues; Tele: Audic, P.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark A;Residues; Tele: Audic, Audic, P.; Pali: Audic, P.; Pali: A; Eugendme, P.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark A;Residues; Tele: Audic, Audic, P.; Pali: A;
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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1328
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Durand, L.; Dussurget, O.; Entlan, K.
  A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlar A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1328
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C;Superfamily: cell division protein ftsZ
                                                                                                                   D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: F83969
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirz R;Takami, Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-division initiation protein (septum formation) ftsZ [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06277.1; GSPDB:GN00
A;Experimental source: strain C-125
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A; Residues: 1-382 <STO>
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C;Superfamily: cell division protein ftsZ
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Pred. No. 7.2e-38;
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                                                                                                                                                                    K.D.;
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                                                                                                                                                                                          P.;
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                                                                                                                                                                    Bloecker
Fsihi, H.
                                                                       Wehland
cell division protein ftsZ homolog - Wolbachia sp. (fragment) C;Species: Wolbachia sp. C;Species: Wolbachia sp. C;Date: 09-Dec-1993 #sequence_revision 12-Apr-1996 #text_change C;Accession: S35264; S35404
                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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D: Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduenok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Listeria innocua (;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AHI699 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, pominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.I.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: itsz
C; Superfamily: cell division protein ftsz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-392 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97368.1; PID:g16414652; GSPDB:GN00178
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A;Molecule type: DNA
A;Residues: 1-391 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell-division initiation protein FtsZ homolog ftsZ [imported] - Listeria innocua (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: cell division protein fts2
155 KEAVDTLIVIPNDRLLQIVDKNTPMLEAFREADNVLRQGVQGISDLIAVPGLINL
                                                    124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                  95 GSDMVFVTAGMGGGTGTGAAPVIAQIAKEMGALTVGVVTRPFGFEGPKRTKQALTGTEAM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 VQGVEFISVNTDAQALNLAKAETKLQIGTKLTRGLGAGAVPEIGKKAAEESREQIEEALK 94
                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                               4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
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                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                VQGVEFISVNTDAQALNLAKAETKLQIGTKLTRGLGAGAVPEIGKKAAEESREQIEEALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEAVDTLIVIPNDRLLQIVDKNTPMLEAFREADNVLRQGVQGISDLIAVPGLINL
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                         57.6%;
56.0%;
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                                                                                                                                                                                                                                                                                                                   35; Mismatches
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                                                                                                                                                                                                                                                                                                                                              Score 510; DB 2;
Pred. No. 3.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                    Length 392;
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Boland, J.A.;
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  209
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Voss, H.; W
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Fsihi,
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Wehla
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26-Aug-1999

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R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: H97108
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Mol. Gen. Genet. 240, 213-220, 1993
A;Title: Cloning and characterization of an ftsz homologue from a bacterial symbiont A;Reference number: S35264; MUID:93360900; PMID:7689140
A;Accession: S35264
A;Accession: S35264
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-398 <HOLD
A;Cross*references: EMBL:X71906; NID:g311274; PIDN:CAA50724.1; PID:g311275
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in lacking 284
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A; Residues: 1-373 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell division GTPase FtsZ [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: H97108
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C;Superfamily: cell division protein fts2
C;Keywords: cell division; GTP binding
F;109-115/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif
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A; Gene: ftsz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAC1693
        155
                                                        124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 IVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 VRRMPIAELGLEELQKYVDTLIVIPNQNLFRIANEKTTFSDAFKLADNVLHIGIRGVTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 PRTTRLANAGVKELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDL 169
                                                                                                                   95
                                                                                                                                       64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 IKDSHMLFITAGMGGGTGTGAAPVIAKAAREARAAVKDRAPKEKKILTVGVVTKPFGFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LQDSNMLFITGGMGGGTCTGAAPVVASVAREL-------GILTVGVVSTPFRSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 SNLQGVNFVVANTDAQALEKSLCDKKIQLGINLTKGLGAGALPDVGKGAAEESIDEIMEH
                                                                                                                                                                                                                                                                               4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM 61
                                                                                                                                                                                                                                                                                                                                                                        Similarity
ERVOTLYTIPNERLLAIVDKKTTLVEAFKSADDVLRQGVQGISDLITIPGLVNL
                                                                                                             GADMVFITAGMGGGTGTGAAPVVAEIAKSMGILTVGVVTKPFPFEGRKRMLHAESGIKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVMPGLINL 224
                                                                                                                                                                                                                          LKNVEFTAINTDKQALALSQASQKIQIGDKLTKGLGAGANPEIGQKAAEESKDEISQAIK 94
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                                                                                                                                                                                                                                                                                                                                                                  57.3%; Score 507; DB 2; 56.0%; Pred. No. 5.4e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
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                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                          42; Indels
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A; Molecule type: DNA
A; Residues: 34-119, A' <RES>
A; Cross-references: EMBL: 212164; NID: 949293; PID: 949294
A; Experimental source: strain 212
C; Comment: This cytoplasmic protein associates with the cell membrane just prior to
                                                                                                                                                                                          R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Keywords: cell division; GTP binding
F;120-126/Region: tubulin/Ftsz GTP/GDP-binding (G-G-G-T-G-[ST]-G)
                                       A; Molecule type: DNA
A; Residues: 1-508 <STO>
                                                                                                                       A;Status:
                                                                                                                                                  A; Reference number: A87249; A; Accession: C87564
                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell division protein Fts2 [imported] - Caulobacter crescentus
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R;Old, I.G.; MacDougall, J.H.; Saint Girons, I.; Davidson, B.E.
FEMS Microbiol. Lett. 99, 245-250, 1992
A;Title: Mapping of genes on the linear chromosome of the bacte
A;Reference number: I40082
A;Accession: I40082
A;Accession: I40082
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A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi
A; Reference number: A70100; MUID:98065943; PMID:9403685
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 26-Aug-1999
C;Accession: C70137; I40082; S21557
C;Accession: C70137; I40082; S21557
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
son, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
A;Cross-references: GB:AE005673; NID:g13424103; PIDN:AAK24511.1; GSPDB:GN00148
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                                                                                                                   preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 MYFITAGMGGGTGTGAAPVIAQVAKELGILTVGVYTKPFKFEGPKKLRLAEQGINNLRKS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 VEFIVANTDLQALQTSIAPIKIALGAKVTAGLGAGGKPEIGQAAAEEDIDVIRNHLSGAD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQDSN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
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A;Cross-references: GB:M22630; NID:g142938; PIDN:AAA22457.1; PID:g142941

R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Hennaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mullo, M.F.
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Auchors: Gomplete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Recession: A69628
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                                                                                                                                                                                                                                                         C;Superfamily: cell division protein ftsz
C;Keywords: cell division; GTP binding
F;106-112/Region: tubulin/Ftsz GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                   th vegetative and sporulating cell divisions
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-382 <KUN>
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C;Superfamily: cell division protein ftsZ1
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A; Residues: 1-382 <RES>
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A; Reference number: 139846; MUID:89008108; PMID:3139638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: This cytoplasmic protein associates with the cell membrane just prior to cel
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                                                                                                                                                                       Similarity
NEVQGVEYIAVNTDAQALNLSKAEVKMQIGAKLTRGLGAGANPEVGKKAAEESKEQIEEA 92
                                                             SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM 61
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53.7%;
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                                                                                                                                     37;
                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                  Score 498;
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                                                                                                                                                                3; DB 1; Length 382; 3.4e-36;
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E86858

cell division protein FtsZ [imported] - Lactococcus lactis subsp. lactis (strain IL14 C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-417 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain IL1403
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156 RANVDTLLIISNNNLLEIVDKKTPLTEALREADNVLRQGVQGVTDLITNPGMINL
                                                        124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                   36 VSGVEFIAANTDVQALRSSKADTVIQLGPKLTRGLGAGAQPEVGKRAAEESAETVSQALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                     64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 LQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVK 121
                                                                                                                                                                                                                                                                                                                  4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63
                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                                                                                                                                           n 55.7%; Score 493; DB 2 Similarity 56.0%; Pred. No. 1e-35;
                                                                                                                      GSDMIFITAGMGGGTGTGAAPVIAQIAKELGALTVGVVTRPFGFEGSKRSYFATEGIEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                             29; Mismatches
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   210
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A;Cross-references: EMBL:AL109663; PIDN:CAB51991.1; GSPDB:GN00070; SCOEDB:ftsZ A;Experimental source: strain A3(2) C;Comment: This cytoplasmic protein associates with the cell membrane just pric C;Genetics:
                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U10879; NID:g4204101; PIDN:AAD10533.1; PID:g527649
A;Experimental source: strain A3(2)
R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Raja
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21563
A;Accession: T34952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;McCormick, J.R.; Su, E.P.; Driks, A.; Losick, R. Mol. Microbiol. 14, 243-254, 1994
A;Title: Growth and viability of Streptomyces coelicolor A;Reference number: $60763; MUID:95131746; PMID:7830569
A;Accession: $60765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell division protein ftsZ - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 27-Apr-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C;Accession: S60765; T34952
                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-399 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-399 <MCC>
                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S60765
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cytoplasmic protein associates with the cell membrane just prior

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A; Description: 1
C; Superfamily: 0
C; Keywords: cel:
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 05-Feb-1999
C;Accession: JE0282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell division protein ftsZ - Streptomyces collinus
C;Species: Streptomyces collinus
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 18-Aug-2000
                                                            probable cell division protein fts2 - Mycobacterium tuberculosis (strain H3 C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-402 <ZHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 249, 556-561, 1998
A;Title: Characterization of ftsz gene and its protein product from Streptomyces A;Reference number: JE0282; MUID:98380301; PMID:9712736
A;Accession: JE0282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Zhulanova, E.; Mikulik, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ftsz
A; Start codon:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                       4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 486; DB 2;
Pred. No. 4.1e-35;
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Search completed: June Job time: 49 secs

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RESULT 15
C97610
Cell division protein ftsz [imported] - Agrobacterium tumefaciens (strain C58, c;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: C97610
C;Accession: C97610
C;Accession: C97610
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A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
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C;Superfamily: cell division protein
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                                                                                                                                                                                                                                                                                                A; Map position: circular chromosome C; Superfamily: cell division protein
                                                                                                                                                                                                                                                                                                                                   A; Gene: AGR_C_3784
                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-583 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A97359; PMID:11743194 A; Accession: C97610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
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A; Residues: 1-379 <COL>
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Best Local
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 158
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                                                                      QKSVDTLIVIPNQNLFRIANDKTTFADAFAMADQVLYSGVACITDLMVKEGLINL
                                     AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                LQGVDFVVANTDAQALTMTKADRVIQLGVNVTEGLGAGSQPEVGRAAAEECIDEIIDHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESCOTLIVIPNDRLLQMGDAAVSLMDAFRSADEVLLNGVQGITDLITTPGLINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GADMVFVTAGEGGGTGTGGAPVVASIARKLGALTVGVVTRPFSFEGKRRSNQAENGIAAL
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ce: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                          GB:AE007869; PIDN:AAK87836.1;
                                                                                                                                                                                                                                       54.5%;
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                                                                                                                                                                                                                                                                                                protein ftsZl
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                                                                                                                                                                                                                          26; Mismatches
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Pred. No. 4.7e-35;
                                                                                                                                                                                                                                       Score 482; DB 2;
Pred. No. 1.4e-34;
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                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                          PID:g15157218; GSPDB:GN00169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity). SUBUNIT: Aggregates to form a ring-like structure (By similarity). SUBCELIULAR LOCATION: Cytoplasmic, Assembles at the inner surface of the cytoplasmic membrane (By similarity). SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL
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                                                                                                                    99;
                                                                                                                                                                                                                                                                                                                                                                            PR00423; CELLDVISFTSZ. s; TIGR00065; ftsz; 1.
                                                                                                                                               Similarity
ANLQGANFVVANTDAQSLEHSLCINKIQLGVSTTRGLGAGASPEVGALAAQESENEIRSS 95
                          MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
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                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                          Septation; GTP-binding; Complete proteome 7 115 GTP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9823893;
                                                                                                                                                                                                                                     48806 MW;
                                                                                                                                            58.5%;
55.9%;
                                                                                                                 38;
                                                                                                                                            Score 518; DB 1; Pred. No. 5.8e-37;
                                                                                                                                                                                                                               D6AC69F28B3343AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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RESULT 3
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00065; ftsZ; 1
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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Nucleic Acids Res. 28:4317-4331(2000).

-!- FUNCTION: This protein is essential to the cell-division process.

It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the circular and the formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell division; Septation; GTP-binding; Complete proteome NP_BIND 104 112 GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001515; BAB06277.1; -. HSSP; Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISFTSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000158; InterPro; IPR003008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the cytoplasmic membrane (By similarity).
-!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9K9T7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=86665;
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                              102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
35 LQGVDFISVNTDAQALHLSKAEVKLQLGGKLTRGLGAGANPEIGKKAAEESREQIEEALQ
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                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENSNMVFITAGMGGGTGTGSAPIIARIAKELGILTVGVVTKPFHFEGGHRMKTADKGLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 40, l (Rel. 40, l) (Rel. 40, l) (Rel. 41,
                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40583 MW;
                                                                                                                                                                                                                                                                                                                                             57.7%; Score 511; DB 1; 58.3%; Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tubulin_FtsZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update) fts2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions on it in no my as its content is in no my wed. Usage has been as the second of the secon
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                                                                                                                                                                                                                                                                                                                                                                                              Length 382;
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                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO00158; Ftsz.
InterPro; IPRO03008; Tubulin_Ftsz.
Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISFTSZ.
TICRFAMS; TIGR00065; ftsz; 1.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X71906; CAA50724.1; -. HSSP; Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holden P.R., Brookfield J.F.Y., Jones P.; "Cloning and characterization of an ftsZ homologue from a bacterial symbiont of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Wolbachieae; Wolbachia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTSZ_WOLSP
P45485;
                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                Cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93360900; PubMed-7689140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

SUBUNIT: Aggregates to form a ring-like structure (By similarity). SUBUNIT: Aggregates to form a ring-like structure (By similarity). SUBURITAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).

SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    division
                                110 PNRTRLANAGVKELAKYVDTLIVVPNONLLALADKSTTMLEAFRYADDVLLEGVKGVTDL 169
                                                                                                                                                                                                                     106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 KEKVDTLIVIPNDRLLEIVDKNTPMLEAFREADNVLRQGVQGISDLIATPGLINL
                                                                                                      62 LQDSNMLFITGGMGGGTCTGAAPVVASVAREL------GILTVGVVSTPFRSEG
                                                                                                                                                                             2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM
                                                                                                                                                                                                                                      Similarity
VRRMPIAELGLEELQKYVDTLIVIPNQNLFRIANEKTTFSDAFKLADNVLHIGIRGVTDL
                                                                                                                                           SNLQGVNFVVANTDAQALEKSLCDKKIQLGINLTKGLGAGALPDVGKGAAEESIDEIMEH
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                                                                      IKDSHMLFITAGMGGGTGTGAAPVIAKAAREARAAVKDRAPKEKKILTVGVVTKPFGFEG
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                                                                                                                                                                                                                                                                                           398 AA;
                                                                                                                                                                                                                     Conservative
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7 115 GTP (POTE
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                                                                                                                                                                                                                                                                                           42497 MW;
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56.1%;
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                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                              Score 510; DB 1;
Pred. No. 2.4e-36;
                                                                                                                                                                                                                                                                                                             GTP (POTENTIAL)
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                        Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: This protein is essential to the cell-division process.

-! FUNCTION: This protein is essential to the cell-division process.

-! Submitted (JUN-1992) to the essential to the colling on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

-! SUBUNIT: Aggregates to form a ring-like structure (By similarity).

-! SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M. van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTSZ_BORBU STANDARD; PRT; 399 AA P45483; Q59183; 01-NOV-1995 (Rel. 32, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
   or send an email
                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93146383; PubMed=1490605;
Old I.G., Macdougall J.H., Saint-Girons I., Davidson B.E.;
"Mapping of genes on the linear chromosome of the bacterium Borrelia burgdorferi: possible locations for its origin of replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 35210 / B31;
Dunn J.J., Butler-Loffredo L., Kieleczawa J.,
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                         of the cytoplasmic membrane (By similarity). SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiol. Lett. 78:245-250(1992).
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to license@isb-sib.ch).
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               Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus.";
                                                                                                                                                                                                                                                                                                                            Quardokus E., Din N., Brun Y.V.;
"Cell cycle regulation and cell type-specific localization of the FtsZ division initiation protein in Caulobacter.";
Proc. Natl. Acad. Sci. U.S.A. 93:6314-6319(1996).
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15-JUN-2002 (Rel. 41, Last annotation
Cell division protein ftsz.
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Quardobine =
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EMBL; AB001137; AAC66649.1; ALT_INIT.
EMBL; AB0885; CAA65464.1; ALT_INIT.
EMBL; L76303; AAB51402.1;
EMBL; Z12164; CAA78156.1; ALT_INIT.
HSSP; Q57816; IFSZ.
TIGR; BB0299; ...
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3 121 GTP (POTENTIAL).
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Pred. No. 5.3e-36;
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RESULT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISTSZ.
TIGRAMS; TIGR00065; ftsZ; 1.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 Cell division; Septation; GTP-binding; NP_BIND 107 115 GTP (POTE)
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q57816; 1FSZ.
TIGR; CC2540; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U40273; AAC44223.1; -. EMBL; AE005922; AAK24511.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubulin_FtsZ.
                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

SUBCLIDUAR LOCATION: Cytoplasmic. Assembles at the inner surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or the cytoplasmic membrane (By similarity). SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                        124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL
                                                                                                                                                                                                                                                                    102;
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                                                                                                                                             DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
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                                                                                                                        GAHMVFITAGMGGGTGTGAAPIIAKCARERGILTVGVVTKPFHFEGRHRMRLADSGIQEL
                                                                                                                                                                                                                                                                                                                                             508 AA;
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                                                                                                                                                                                                                                                                                   57.1%; Score 505; DB 1; 58.3%; Pred. No. 8.5e-36;
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G -> A (IN REF.
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FTSZ_BACSU
                                                  MEDLINE=89008108; PubMed=3139638; Beall B., Lowe M., Lutkenhaus J.; Beall B., Lowe M., Lutkenhaus J.; Beall B., Lowe M., Lutkenhaus J.; Becherichia coli cell division genes ftsz and ftsA."; J. Bacteriol. 170:4855-4864(1988).
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01-DEC-1992 (Rel. 24,
15-JUN-2002 (Rel. 41,
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STRAIN-168;
                SEQUENCE FROM N.A.
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                                                                                                                                                                                                             Bacteria; Firmicutes;
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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Llu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Llu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Meliado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Scrokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Tarshashi H., Takemaru K.,
RA Tasato V., Uchiyama S., Vandenbol M., Vannier F., Vasarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Baciilus
"Te subtilis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M22630; AAA22457.1;
EMBL; 29911; CAB13402.1;
EMBL; 205400; AAA83361.1;
HSSP; Q57816; 1FSZ.
Subtilist; BG10232; ftsZ.
                                                                                                                                                             Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISTSZ.
TIGRFAMS; TIGR00065; ftsz; 1.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000158; Ftsz.
InterPro; IPR003008; Tubulin_Ftsz.
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120ning, genetic organization, and characterization of a structural
121ning, genetic organization, and characterization of a structural
121ning, genetic organization, and characterization of a structural
121ning bacillopeptidase F from Bacillus subtilis.";
132ning bacillopeptidase F from Bacillus subtilis.";
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172ning bacillus surface of the cytoplasmic membrane at the place where division will occur,
172ning bacillopeptidase form a ring is the signal for septation to
172ning bacillopeptidase form a ring-like structure (By similarity)
172ning bacillus surfaces of bacillopeptidase form a ring-like structure (By similarity)
172ning bacillopeptidase form and bacillus subtilision form a ring-like structure (By similarity)
172ning bacillopeptidase form and bacillopeptidase form and bacillus subtilision form and ba
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                                                                                                                division;
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15-DEC-1998
15-JUN-2002
                                                  PROSITE; PS011:
Cell division;
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                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed
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SEQUENCE
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                             NP_BIND
                                                                                                            PROSITE;
                                                                                                                                                                    PRINTS; PRO0423;
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InterPro; IPR003008; Tubul
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                                                                                                                                          TIGRFAMS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (APR-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity). SUBUNIT: Aggregates to form a ring-like structure (By similarity). SUBCLIDITAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic assembles at the inner surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the cytoplasmic membrane (By similarity). SIMILARITY: BELONGS TO THE FTSZ FAMILY.
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                                                                               PS01134; FTSZ_1; PS01135; FTSZ_2;
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                                                                                                                                    R00423; CELLDVISFTSZ.
TIGR00065; ftsZ; 1.
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592 AA;
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(Rel. 37, Last seq
(Rel. 41, Last ann
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                             107
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63503 MW;
                                                                                                                                                                                                                                                                                                                                                                                           license agreement (See http://www.isb-sib.ch/announce/
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                          GTP (POTENTIAL)
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Pred. No. 2.5e-35;
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C32007DADCD2D75B CRC64;
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Query Match

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008458;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last seq

15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                    PROSITE; PS01134; FTSZ_1; 1. PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                        PRINTS; PR00423; CELLDVISFTSZ.
TIGRFAMS; TIGR00065; ftsz; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Duez C., Thamm I., Sapunaric F., Coyette J., Ghuysen J.-M.;
"The division and cell wall gene cluster of Enterococcus hirae
DNA Seq. 9:149-161(1998).
                                                                                                                                                                                                                                                                                                InterPro; IPR003008; Tubulin_FtsZ.
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y13922; CAA74240.1; HSSP; Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
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                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity). SUBURIT: Aggregates to form a ring-like structure (By similarity). SUBCELLULAR LOCATION: Cytoplasmic, Assembles at the inner surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the cytoplasmic membrane (By similarity). SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158
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  97; Conser
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                                                                                                         413 AA;
  Conservative
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                                                    Score 492;
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-!- SUBUNIT: Aggregates to form a ring-like structure (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).
-!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell division; Septation; GTP-binding.
NP_BIND 105 113 GTP (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01134; FTSZ_1; FALSE_NEG. PROSITE; PS01135; FTSZ_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMs; TIGR00065; fts2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubulin_FtsZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A24836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTSZ_ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to
124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL 210
                                                           96 GADMIFITAGMGGGTGTGAAPVVAKIAKELGALTVGVVTRPFSFEGPKRGRFAAEGIALL
                                                                                       64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                                                                                                                                              36 VKGVEFITANTDVQALKHSKAETVIQLGPKYTRNLGAGSQPEVGQKAAEESEQVISESLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                       4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
                                                                                                                                                                                                                                                                                                     99;
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GADMIFITAGMGGGTGTGAAPIVAGIAKELGALTVGVVTRPFTFEGPKRGRFAAEGIARL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKGVEFITANTDVQALKNSKAETVIQLGPKYTRGLGAGSQPEVGQKAAEESEQALREALD 95
                                                                                                                                                                                                                                                                                                                                                                                                                            412 AA;
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                                                                                                                                                                                                         44355 MW;
                                                                                                                                                                                                                                                                                                                              55.3%; Score 489; DB 1; 56.6%; Pred. No. 1.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Streptococcus faecalis)
Lactobacillales; Enteroc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftsZ.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            42EA85BAA70EF51F CRC64;
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
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tent is in
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RESULT 12
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Best Local
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF273451; AAF78784.2; HSSP; Q57816; 1FSZ. InterPro; IPR000158; FtsZ. InterPro; IPR003008; Tubulir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell division protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYCKA
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00423; CELLDVISFTS2.
TIGREAMS; TIGR00065; ft82; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium kansasii.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01134; FTSZ_1; 1. PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTSZ_MYCKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was by non-profit institutions as long as its content is in no was by non-profit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

SUBUNIT: Aggregates to form a ring-like structure (By similarity). SUBCELULLAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).

SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 KENVDTLLIISNNRLLEVVDKKTPMLEAFREADNVLRQGVQGISDLITAPGYVNL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00091; tubulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene of M. kansasii.";
                                                                                                                                                                                      64
                                                                                                                                                                                                                                        4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                    AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                     LKGVEFIAINTDAQALLMSDADVKLDVGRDSTRGLGAGADPEVGRXAAEDAKDDIEELLR
                                                                                    RESCOTLIVIPNDRLLQMGDAAVSLMDAFRSADEVLLNGVXGITDLITTPGLINV
                                                                                                                                                   GADMVFVTAGEGGGTGTGGAPVVASIARKLGALTVGVVTRPFSFEGKRRSNQAENGIQAL
                                                                                                                                                                                                                                                                                                                                                     386 AA;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Septation; GTP-binding.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                       39051 MW;
                                                                                                                                                                                                                                                                                                      54.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tubulin_FtsZ.
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Last annotation updat
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ω
                                                                                                                                                                                                                                                                                                                                                                       GTP
                                                                                                                                                                                                                                                                                                     Score 486; DB 1;
Pred. No. 2.6e-34;
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                       P (POTENTIAL).
215DE0B814EED593 CRC64;
                                                                                                                                                                                                                                                                                       Mismatches
     399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386
                                                                                                                                                                                                                                                                                                                  DB 1; Length 386;
     À
                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration -
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32

LKGVEFIAINTDAQALLMSDADVKLDVGRELTRGLGAGANPAVGRKAAEDHREEIEEVLK

91 63

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Matches
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                   PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).

Nature 417:141-147(2002).

It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

SUBCHILIULAR LOCATION: Cytoplasmic, Assembles at the inner surface of the cytoplasmic membrane (By similarity).

SUBLIBITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quali M.A., Kieser H. Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P455U0;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                 InterPro; IPR000158; Ftsz.
InterPro; IPR003008; Tubulin_Ftsz.
Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISPTSz.
TIGRFAMS; TIGR00065; ftsz; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U10879; AAD10533.1; -. EMBL; AL109663; CAB51991.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Microbiol. 14:243-254(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95131746; PubMed=7830569; MCCOrmick J.R., Su E.P., Driks A., Los "Growth and viability of Streptomyces division gene ftsz.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell division protein ftsz. FTSZ OR SC02082 OR SC4A10.15c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P45500;
01-NOV-1995
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; Q57816; 1FSZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                     division;
4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
                                                                                           Similarity
                                                                                                                                                                                                                                                                PS01134; FTSZ_1; PS01135; FTSZ_2;
                                                                                                                                                                              101
399 AA;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M145;
                                                                                                                                                                                                         Septation; GTP-binding; Complete proteome 1 109 GTP (POTENTIAL).
                                                                                                                                                                                 41095 MW;
                                                                                        54.9%;
53.1%;
                                                          38;
                                                                                           Pred.
                                                                                     Score 486; DB 1;
Pred. No. 2.7e-34;
                                                                                                                                                                              EAD52804CFBB4D39 CRC64;
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Losick R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor mutant for the cell
                                                                                                                    Length 399;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins M.,
Howarth S.,
                                                             0
                                                          Gaps
                                                             <u>.</u>
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RX MEDLINE=8829597; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davles R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Hornsby T., Jagels K., Krogh A., Rajandream M.A., Rogers J.,

RA ROILer S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

NA Laure 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  TubercuList;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L:, White.O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bishai W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinoycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell division protein ftsz.
FTSZ OR RV2150C OR MT2209 OR MTCY270.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, 15-JUL-1998 (Rel. 36, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTSZ_MYCTU
O08378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                             It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By Similarity).

SUBUNIT: Aggregates to form a ring-like structure (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).

SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This protein is essential to the
                                                                                               Z95388; CAB08643.1;
                                                                           AE007068;
                                                     Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRDGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123
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                  Rv2150c;
                                                                       AAK46493.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-division process
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IPR000158; FtsZ

Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISTTSZ.

TIGR00065;

InterPro; IPR000158; InterPro; IPR003008;

Tubulin_FtsZ

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RESULT 14
FTSZ_STRG
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Best Local
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                    EMBL; U07344; AAA56889.1; HSSP; Q57816; 1FSZ.
                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dharmatilake A.J., Kendrick K.E.)
"Expression of the division-controlling gene fts2 during growth and sporulation of the filamentous bacterium Streptomyces griseus.", Gene 147:21-28(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRING, TIGROOUS; TIGROOUS; TIGROMS; TIGROOUS; TIGROMS; TIGROOUS; T
                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                    of the cytoplasmic membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NRRL B2682;
MEDLINE=94374704; PubMed=8088545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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TIGREAMS; TIGR00065; ftsZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003008; Tu
Pfam; PF00091; tubulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: This protein is essential to the cell-division process. It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

SUBCHIT: Aggregates to form a ring-like structure (By similarity).

SUBCHITLAR LOCATION: Cytoplasmic. Assembles at the inner surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRGR
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                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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54.3%;
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Pred. No. 3.1e-34;
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                                                                                                                                                                                                                                                                                                   as its content
                                                                                                                                                                                                                                                                      Usage
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: OM protein - protein search, using sw model

June 2, 2003, 06:27:41; Search time 72 Seconds (without alignments) 509.394 Million cell updates/sec

Title: Perfect score: Sequence: US-09-770-509-2 885 1 ASQLEGVEFIVANT ASQLEGVEFIVANTDCQALG.....LLEGVKGVTDLIVRPGLINL 178

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_21:*

Sp_archea:*

sp_archea:*

sp_fungi:*

sp_fungi:*

sp_human:*

sp_manmal:*

sp_manmal:*

sp_manmal:*

sp_manmal:*

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sp_pane:* sp_archea:*
sp_bacteria:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_phage: * sp_organelle:* sp_rodent:*
sp_virus:* sp_plant:*

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_vertebrate:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score 547	Query Match	Length DB	2	ID Q8RMK5
N F	527	59.5	336	N	Q9RNN2
ω	527	59.5	401	10	Q9M7M6
4	525	59.3	421	N	Q9AQ38
G.	524	59.2	452	N	Q9AQ36
6	521	58.9	400	N	Q9AQ37
7	520	58.8	357	16	Q8R9H2
8	520	58.8	370	N	085474
9	517	58.4	231	N	P77997
10	517	58.4	289	N	008390
11	515	58.2	289	N	008392
12	514	58.1	289	N	008471
13	514	58.1	289	N	008389
14	514	58.1	289	N	008391
15	510	57.6	391	16	08Y5M5
16	510	57.6	200		

52.	52.	53.	53.	53.	53.	53.	53.	53.	54.	54.	54.	54.	54.	55.	55.	55.	55.	55.	55.	55.	55.	55.	55.	56.	56.	56.	503 56.8	57.
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Q9evs0		Q9evs3	Q9z3b8	9	Q9zhb9	Q93ta1	Q8y160	N	Q9rme1	Q8udn5				086036	Q98kb9		09f1m6		Q916v2		Q9ceh2	085475	Q8xjj1				9074	Q971e9
wolbachia s	wolbachia s	wolbachia s	wolbachia s	streptococc	streptococc	brucella ab	brucella me	rhizobium l	acholeplasm	agrobacteri	wolbachia e	streptomyce	epulopisciu	wolbachia e	rhizobium l	lactococcus		cyanidiosch	wolbachia e	ε	lactococcus	13	clostridium	bartonella	wolbachia e	bartonella	bartonella	clostridium

## ALIGNMENTS

Qy	рb	Qy	ф	Qy	Ma Ma	so	편 (	DR RL	RT	RT :	R.	Z 2	3 7	J Z	2	8	ጸ	20	GN	DE	ğ ξ	7 5	₹ A	Đ	Q8RMK5	RESULT
122 ELAKYYDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178	96 LEGANMVFITAGMGGGTGTGAAPVIARAARERGLLTVGVVTKPFHFEGAHRMRLAESGIA 155	62 LQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVK 121	36 SNLEGVDFVVGNTDAQALKGSLCEKRVQLGTTMTRGLGAGSKPDVGRASAEEQLEEIIGH 95	2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM 61	Query Match 61.8%; Score 547; DB 2; Length 253; Best Local Similarity 60.5%; Pred. No. 2.9e-41; Matches 107; Conservative 30; Mismatches 40; Indels 0; Gaps 0;	SEQUENCE 253 AA; 26638 MW; 13B8B38B0AF4702D CRC64;	NON TER OSS OSS OSS	Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.	and maize root colonization.";	brasilense is altered in exopolysaccharide production, salt tolerance,	"A ddlB (D-alanine-D-alanine ligase) TnS mutant of Azospirillum	JIRAINELD LAGATES A MOTI G R	SEQUENCE MICH N.A.	EDITENCE FROM N	NCBI_TaxID-192;	Azospirillum.	Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;	Azospirillum brasilense.		on protein FtsZ (	01-JUN-2002 (Trembirel, 21, Last annotation update)	(Prevent of of		QURMK5 PRELIMINARY; PRT; 253 AA.		IJT 1

ELQQYVDTLIIIPNQNLFRIANEKTTFADAFKMADDVLHSGVRGVTDLMVMPGLINL

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RESULT OF REAL OF REAL
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                                                                                                                                                                                                                                                                                                                                     RESULT 3
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Best Local
                                                                                               01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Cell division protein ftsz.
FTSZ OR MSFTSZ-MT.
                                              Eukaryota; stramenopiles; Chrysophyceae;
                                                                                 Mallomonas splendens.
                                                                                                                                                                                                                                              Q9M7м6;
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PRINTS; PR00423; CELLDVISETSZ.

TIGRAMS; TIGR00065; ftsz; 1.

PROSITE; PS01134; FTSZ_1; 1.

PROSITE; PS01135; FTSZ_2; 1.

Cell division; GTP-binding; Septation.

SEQUENCE 336 AA; 35725 MW; 8CEFFIF7150436C7 CRC64;
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Q9RNN2;
01-MAY-2000
                    NCBI_TaxID=52552;
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-!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
EMBL; AF179611; AAD53930.1; --
HSSP; Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of 41E10 fosmid clone of Zymomonas mobilis.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
-ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN.
                                                                                                                                                                                                                                                                             Q9м7м6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000158; Ftsz.
InterPro; IPR003008; Tubulin_Ftsz.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Om H.W., Kang H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zymomonas mobilis.
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SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY)
SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTDFRSEGDNRTRLANAGV 120
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                                                                                                                                                                                                                                                                                                                                                                                                             EELQKHVDTLIVIPNQNLFLIANPNTTFKQAFQMADEVLQQGVRGITDLMVCPGLINL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASGVQGVDFIVANTDAQALNISPAEQRIQLGPTTTQGLGAGSRPEVGKAAAEETIEQIQE 97
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                                                                                                                                                                                                                                                                           PRELIMINARY;
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59.6%;
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Last sequence update)
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                                                                                                                                                                                                                                                                        PRT;
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                                                 Synurales; Mallomonas
                                                                                                                                                         update)
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Best Local
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InterPro; IPR003008; Tubulin_Ftsz.
Pfam; PP00091; tubulin; 1
PRINTS; PR00423; CELLDVISTTSz.
TIGRFAMS; TIGR00065; ftsz; 1.
PROSITE; PS01135; FTSZ_2; 1.
Cell division; GTP-binding; Septation.
SEQUENCE 401 AA; 42337 MW; E7B6A08C
            -i- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY)
-i- SUBCELLULAR LOCATION: CYTOPLEASHLE ASTEMBLE AT THE INNER SURFACE
OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                    Lee K.N., Massung R.F., Padmalayam I., Baumstark B.; "Characterization of the ftsz gene in Ehrlichia chaffeen agent and Ricketttsia rickettsii"; submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2002 (TrEMBLrel. 21, Cell division protein ftsz.
 EMBL;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Anaplasmataceae;
                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AQ38;
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                                                                                                                                                                                                                                                                             NCBI_TaxID=945
                                                                                                                                                                                                                                                                                                                                 Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE FTSZ FAMILY. EMBL; AF120116; AAF35432.1; -.
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                                                                                 FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS. ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SUFFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE MHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS. IT IS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

SUBCULTULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF THE CYTOPLASMIC MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KELAKYVDTLIVVPNQNLLALADKSTIMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 YIADANMYFITAGMGGGTGTGAAPVVAEVCMEKDILTVAVVTKPFSFEGKHRARLANEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 ARKLSGVEFVCANTDAQHLSTCLTENKLQLGKESTQGLGCGANPESGRRAAEESKEEIAR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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 AAK00615.2;
                                                                                                                                                                                                                                                                                               Ehrlichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
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Pred. No. 3.3e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
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RESULT 5

ID 09A036

ID 09A036

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DT 01-J

DT 01-J
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                         Query Match
Best Local Similarity
Matches
                                                                                                                                                                     EMBL; AF221946; AAK00617.1; -.
HSSP; Q57816; 1FSZ.
InterPro; IPR000158; FtSZ.
InterPro; IPR003008; Tubulin_FtSZ.
Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISFTSZ.
TICRFAMS; TIGR00065; ftSZ; 1.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9AQ36 PRELIMINARY; PRT; 452 AA.
O9AQ36; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     BEGIN. BINDS TO AND HYDROXIZES GTP (BY SIMILARITY).

-1- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC BURBEANE (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE FTSZ FAMILY.

EMBL, AF221946; AAK00617.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee K.N., Massung R.F., Padmalayam I., Baumstark B.;

"Characterization of the fts2 gene in Ehrlichia chaffeensis, the HGE
agent and Rickettsia rickettsii.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

-ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF
THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
Cell division; GTP-binding; Septation.
Cell division; GTP-binding; Septation.
SEQUENCE 421 AA; 45664 MW; E73CE4B1536255FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00423; CELLDVISFTS2.
TIGRFAMs; TIGR00065; fts2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubulin_FtsZ.
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell division protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia rickettsii.
                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettslaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ELAKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                              division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107;
100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 ISDSNMLFITAGMGGGTGTGAAPVIARVAKENKILTIGVVTKPFHFEGAHRMRTAEFGLE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lon; GTP-binding; Septation 452 AA; 48365 MW; 5DCE41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsieae;
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                             59.2%; Score 524; DB 2; 56.2%; Pred. No. 7.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
   38;
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                                                                                                                           5DCE41568630EBE0 CRC64;
      Mismatches
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                                                             Length 452;
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   Indels
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ASQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQR

60

Q8R9H2

Q8R9H2;

Q8R9H2

PRELIMINARY;

PRT;

357 AA

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RESULT 6
Q9AQ37
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RESULT 7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell division protein fts2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9AQ37
                                                                                                                                                                                                                                                                                                                                                                                                 OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
-|- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
EMBL; AF221945; AAKOO616.1; -.
HSSP; O57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anaplasmataceae; Anaplasma
                                                                                                                                                                                                                                                                      PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
Cell division; GFP-binding; Septation.
SEQUENCE 400 AA; 42001 MW; CDE8730
                                                                                                                                                                                                                                                                                                                            PRINTS; PR00423; CELLDVISFTSZ.
TIGRFAMs; TIGR00065; ftsZ; 1.
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00091; tubulin;
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubulin_FtsZ.
                                                                                                                                                                                                                            Local
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                                        156 ELQKHVDTLIVIPNQNLFRIANENTTFADAFKLADTVLHTGVRGITDLMVMPGLINL 212
                                                                   122 ELAKYVDTLIVVPNONLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 YLENSNMVFITAGMGGGTGTGSAPVIARIAKELGILTVGVVTKPFHFEGGHRMKTADKGL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MLQDSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 SANLQGANFYVANTDAQSLEHSLCTNKIQLGVSTTRGLGAGASPEVGALAAQESESEIRN 94
                                                                                                 96 ISDSNMLFITAGMGGGTGTGAAPVIAKAAKDSKILTVGVVTRPFHFEGAHRMKTAEYGLE
                                                                                                                           62 LODSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVK 121
                                                                                                                                                       36 SCLQGVNFVVANTDAQALDCSLSEKKIQLGMNLTKGLGAGSLPEIGRGAAEESIEEIIAE 95
                                                                                                                                                                                                                105;
                                                                                                                                                                                 2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM 61
                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                            58.9%; Score 521; DB 2; Length 400; 59.3%; Pred. No. 1.1e-38;
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                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                         CDE8730E876FDC9B CRC64;
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Pfam; PF00091; tubulin; 1. PRINTS; PR00423; CELLDVISFTSZ.

Length 370;

Indels

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Gaps

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154

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                                                           POLYSPOTA.";

PIOC. MATI. ACAd. Sci. U.S.A. 95:10218-10223(1998).

-!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IN THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GIF (BY SIMILARITY).

BEGIN. BINDS TO AND HYDROLYZES GIF (BY SIMILARITY).

-!- SUBCULULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                  STRAIN-ATCC49066;
STRAIN-98374332; PubMed-9707627;
MEDLINE-98374332; PubMed-9707627;
Annert E.R., Losick R.M.;
                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2002 (TrEMBLrel. 21, Cell division protein ftsz.
                               HSSP; Q57816; 1FSZ
                                           EMBL; AF067822;
                                                                                                                                                                                                        "Propagation by sporulation in the guinea pig symbiont Metabacterium
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           Clostridium lentocellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                 085474;
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"A complete sequence of T. tengcongensis genome."; Genome Res. 12:689-700(2002).
EMBL; AEC13119; AAM24841.1; ...
                InterPro;
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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01-JUN-2002
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                                                     SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKYVDALITIPNDRLLQVVEKKTSMLDAFKLADDVLRQGVQGISDLIAVPGLVNV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GADMIFITAGMGGGTGTGAAPVVAEIAKELGILTVGVVTKPFTFEGRKRMAQAEMGIEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKGVEFIAINTDKQALSLSKAETKIQIGEKLTKGLGAGANPEIGKKAAEESREEIERAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
IPR003008; Tubulin_FtsZ.
              IPR000158; FtsZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 AA; 37777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / JCM11007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTPase.
                                           AAC32265.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.88;
                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium group; Clostridia;
                                                        TO THE FTSZ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          370 AA.
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Ma Y., Lir
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106;
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PROSITE; PS01134; FTSZ_1; 1.

PROSITE; PS01135; FTSZ_2; 1.

CCl division; GTP-binding; Septation PRINTS; PR00423; CELLDVISFTSZ. InterPro; IPR003008; Tubulin_Ftsz.
Pfam; PF00091; tubulin; 2. EMBL; U37260; AAC44314.1; HSSP; Q57816; 1FSZ. InterPro; IPR000158; FtsZ -1- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY) 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cell division protein ftsZ (Fragment) -!- SIMILARITY: BELONGS TO THE FTS2 FAMILY SEQUENCE FROM N.A.
MEDLINE=96392953; PubMed=8799741; Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; TIGREAMS; TIGRO0065; ftsz; 1.

PROSITE; PS01134; FTSZ_1; 1.

PROSITE; PS01135; FTSZ_2; 1.

Cell division; GTP-binding; Septation SEQUENCE 370 AA; 39449 MW; E7EB1B OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY). BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY) 155 KONVDTLVVIPNDKILQVIDKKTTMVDAFSKADDVLQQGVQGITDLISNPGIINL 95 GADMLFITAGMGGGTGTGAAPVIASIAKEEGILTVGVVTKPFSFEGRKRMINAEKGIAEL 64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL 123 Similarity 4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ 63 Similarity LEGVEFITVNTDHQALARSGAPAKIQIGEKMTRGLGAGANPEIGTKSAEESREEILTAIK 94 231 231 AA; Conservative Conservative PRELIMINARY; Wolbachieae; 24428 MW; 58.4%; Score 517; DB 2; 56.1%; Pred. No. 1.3e-38; 58.8%; 58.9%; 31; 30; Wolbachia Score 520; DB 2; Pred. No. 1.3e-38 3BCB3F6C9DE936E0 CRC64; PRT; Mismatches E7E81B612A992586 CRC64; Mismatches 231 A 42;

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2 SQLEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRM 61 | :|| | :|| | :|| :|| :|| :|| :||

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HSSP; Q57816; 1FSz.
InterPro; IPR000158; Ftsz.
InterPro; IPR003008; Tubulin_Ftsz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jager C.R., Pintureau B., Heddi A.;

"Comparison between phylogenetic trees of some Trichogramma species and their Wolbachia endosymbionts.";

Russ. Entomol. J. 7:163-168(1998).

-I- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

-I- SUBCULLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cell division protein ftsz (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO0065; ftsZ; 1. PROSITE; PS01134; FTSZ_1; 1. PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISFTSZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-59580;
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                    110 PNRTRLANAGVKELAKYVDTLIVVPNQNLLALADKSTIMLEAFRYADDVLLEGVKGVTDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           division; GTP-binding; Septation.
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289 AA;
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RESULT 12
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pfam; pF00091; tubulin; 1
PRINTS; PR00423; CELLDVISETSZ.
TIGRPAMS; TIGR00065; ftsz; 1
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
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-!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
-ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
-!- SUBGULIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Rickettsiaceae; Wolbachieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                    122 VRRMRTAELGLEELQKYVDTLIVIPNQNLFRIANEKTTFADAFQLADNVLHIGIRGVTDL
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      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B., Heddi A.;
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ae; Wolbachia.
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         PRT;
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RAY Jager C.R., Pintureau B., Heddi A.;

STRAIN-M36, AND 1148;

RI Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

CC :- FURCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

CC ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,

CC AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO

CC BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

CC BEGIN. BINDS TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

CC -!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

CC OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).

CC OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).

CC OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).

CC MBL; U95754; AAB54072.1; -.

DR HSSP; O57816; 1FS2.

DR INTERPO; IPRO030158; FtsZ.

DR INTERPO; IPRO030158; Tubulin_FtsZ.
                                                                                   008389 PKELLILLI

008389; OTTEMBLEEL 04, CI

01-JUL-1997 (TERMBLEEL 04, LI

1 01-JUN-2002 (TERMBLEEL 21, LI

1 01-JUN-2002 (TERMBLEE
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                    Wolbachia sp. 1032.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Wolbachieae; Wolbachia.
NCBI_TaxID=59578;
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PROSITE: PS01134; FTSZ 1; 1.

PROSITE: PS01135; FTSZ 2; 1.

Cell division: CTD-himai
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01-JUL-1997 (TrEMBLrel. 04, Last seque)
01-JUN-2002 (TrEMBLrel. 21, Last annot Cell division protein ftsz (Fragment).
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PRINTS; PR00423; CELLDVISFTSZ.
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NCBI_TaxID=956;
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01-JUL-1997
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289 AA;
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                 Wolbachieae;
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56.1%;
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Last annotation updat
                                                                                                                                                                                        Created)
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Pred. No. 3.2e-38;
29; Mismatches 42
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Last annotation updat
               Wolbachia
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                                      Rickettsiales;
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Jager C.R., Pintureau B., Heddi A.;
"Comparison between phylogenetic trees
and their Wolbachia endosymbionts.";
Russ. Entomol. J. 7:163-168(1998).
-i- FUNCTION: THIS PROTEIN IS ESSENTIAL
ITS SEEMS TO ASSEMBLE INTO A DYNAMI
                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cell division protein ftsZ (Fragment).
                                                                                                                             Wolbachia sp. MB35.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
                                                                             STRAIN-MB35;
                                                                                                                                                                                                                       008391;
01-JUL-1997
                                                                                                                                                                                                                                                008391
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PROSITE; P
                                                                                         SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=59581;
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PRUSS. Entomol. J. 7:163-168(1998).

I'F FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

I'S SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SEQUENCE FROM N.A.
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InterPro; IPR003008; Tubul
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                                                                                                                                                                                                                                                PRELIMINARY;
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56.1%;
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  ESSENTIAL TO A DYNAMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 514;
Pred. No. 3.
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1.2e-38;
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  õ
                                                 Trichogramma
             CELL-DIVISION PROCESS
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SURFACE
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Q8Y5M AC Q8Y5M AC Q8Y5M AC Q8Y5M AC Q8Y5M AC Q8Y5M DT 01-MA DT 01-JU DT FTS2.
GN FTS2.
GN FTS2.
GN ETS2.
GN ETS3.
RA STRAI
RA Glase
RA Gla
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AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
BEGIN, BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
C-I-SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
C-I-SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
COF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
C-I-SIMILARITY: BELONGS TO THE FTSZ FAMILY.
DR HSSP; Q57816; 1FSZ.
DR HSSP; Q57816; 1FSZ.
DR HSSP; Q57816; 1FSZ.
DR HSSP; Q57816; TSZ.
DR HSSP; Q57816; TSZ.
DR PFAMI; TIGRO0065; Ttbullin; 1.
DR PRINTS; PRO0423; CELLDVISETSZ.
DR TIGREAMS; TIGRO0065; ftsZ; 1.
DR PROSITE; PS01134; FTSZ_2; 1.
EMBL GTP-binding; Septation.
EMBL GTP-binding; Septation.
                  RC STRAIN-EGD-E / SEROVAR 1/2A;

RM MEDILINE-21537279; pubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

RA Domann E., Dominguez-Bernal G., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kunn M., Kunst F., Kurapkat G.,

RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Science 294:849-852(2001).
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Best Local S
Matches 106
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Q8Y5M5;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Clostridium Listeriaceae; Listeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 MIMPGLINL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQDSNMLFITGGMGGGTCTGAAPVVASVAREL-------GILTVGVVSTPFRSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNLQGVNFVVANTDAQALEKSLCDKKIQLGINLTKGLGAGALPDIGKGAAEESIDEIMEH
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(TrEMBLrel. 20,
(TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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Search completed: June Job time: 85 secs
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                                                                                                                                                                                                                                                                                 InterPro; IPR000158; Ftsz.
InterPro; IPR003008; Tubulin_FtsZ.
Pfam; pr00091; tubulin; 1.
PRINTS; PR00423; CELLDVISFTSZ.
TIGREAMS; TIGR00065; ftsz; 1.
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                Complete proteome.
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                                                                                                                                                                                                    Local
                                               155
                                                                   124 AKYVDTLIVVPNQNLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                         35
                                                                                                                                                    Similarity
                                                                                                                                        VQGVEFISVNTDAQALNLAKAETKLQIGTKLTRGLGAGAVPEIGKKAAEESREQIEEALK 94
                                             KEAVDTLIVIPNDRLLQIVDKNTPMLEAFREADNVLRQGVQGISDLIAVPGLINL 209
                                                                                                                                                                                                                                                             PS01134; FTSZ_1; 1. PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                      391 AA; 41350 MW;
                                                                                                                                                                                        Conservative
            ν
                                                                                                                                                                                                    57.6%;
            2003, 08:41:12
                                                                                                                                                                                      35; Mismatches
                                                                                                                                                                                                 Score 510; DB 16;
Pred. No. 1.1e-37;
                                                                                                                                                                                                                                      6B9F75B2B1629C58 CRC64;
                                                                                                                                                                                        42;
                                                                                                                                                                                                               Length 391;
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Best Local (
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030992;
                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

1. SUBURIT: Aggregates to form a ring-like structure (By similarity).

1. SUBCELLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).

1. SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGRTU
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PROSITE; PS01135; FTSZ_2; 1.
Cell division; Septation; GTP-binding.
NP_BIND 101 109 GTP (POTENTIAL)
SEQUENCE 407 AA; 41809 MW; 01D2898E01322
                                                InterPro; IPR003008; Tubulin_FtsZ.
Pfam; PF00091; tubulin; 1.
PRINTS; PR00423; CELLDVISTTSZ.
TIGREAMS; TIGR00065; ftsZ; 1.
PROSITE; PS01134; FTSZ_1; 1.
                                                                                                                                    EMBL; AF024659; AAC45821.1; -. HSSP; Q57816; 1FSZ. InterPro; IPR000158; Ft8Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 179:6788-6797(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98012980; PubMed-9352931;
Ma X., Sun O., Wang R., Singh G., Jonietz E.L., Margolin W.;
"Interactions between heterologous FtsA and FtsZ proteins at the FtsZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTSZ.
                              PROSITE; PS01134; FTSZ_1; PS051135; FTSZ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell division protein fts2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhizobiaceae;
                division;
                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 REEVDTLIVIPNDRLLSISDRQVSVLDAFKSADQVLLSGVQGITDLITTPGLINL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 GADMVFVTAGEGGGTGTGRAPVVANIARSLGALTIGVVTRPETFEGRRRANQAEDGIAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 LKGVEFIAINTDAQALLMSDADVKLDVGRELTRGLGAGANPAVGRKAAEDHREEIEEVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LEGVEFIVANTDCQALGRSLAPHKITLGKDITKGLGAGSKPELGKRSAEQQKVDIQRMLQ
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                Septation; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.8%; Score 485; DB 1; 53.1%; Pred. No. 3.4e-34;
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GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01D2898E013220C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583
                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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Job time :
 Search completed: June Job time : 28 secs
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Best Local S
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                                                                                        124 AKYVDTLIVVPNONLLALADKSTTMLEAFRYADDVLLEGVKGVTDLIVRPGLINL 178
                                                                                                                                                                                                                                                 100;
                                                                                                                       98 GTHMCFVTAGMGGGTGTGAAPVVAQAARNKGILTVGVVTKPFHFEGGRRMRLAEQGIEEL
                                                                                                                                                                                  38 LQGVDFVVANTDAQALTMTKADRVIQLGVNVTEGLGAGSQPEVGRAAAEECIDEIIDHLN
                                                                                                                                                                                                 Similarity
                                                                                                                                          DSNMLFITGGMGGGTCTGAAPVVASVARELGILTVGVVSTPFRSEGPNRTRLANAGVKEL
                                                             QKSVDTLIVIPNQNLFRIANDKTTFADAFAMADQVLYSGVACITDLMVKEGLINL
                                                                                                                                                                                                                                                                                                             583 AA;
                                                                                                                                                                                                                                               Conservative
                2, 2003, 08:39:32
                                                                                                                                                                                                                                                                                                             61936 MW;
                                                                                                                                                                                                                                                              54.5%; Score 482; DB 1 57.1%; Pred. No. 9e-34;
                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                             3F415EB5FBCAA1CB CRC64;
                                                                                                                                                                                                                                                 Mismatches
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Command line parameters:

+MODEL-frame+_D2n.model -DEV=xlh
-Q-cgn2_1/USPTQ_Spool_VE09770509/runat_27052003_083648_18820/app_query.fasta_1.327
-DB-GenEmbl -QFMT-fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cd1 -LIST=45
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX-100 -THR_WIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=200000000
-USER=US09770509_@CGN_1_1_2496_@runat_27052003_083648_18820 -NCPU=6 -ICPU=3
-NQ_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAXT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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885
2054640 seqs, 14551402878 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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29: em_vi:*
30: em_tg_hum:*
31: em_htg_lov:*
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33: em_htg_pals:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_rod:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3824 bp DNA linear BCT 11-APR-2002 Azospirillum brasilense D-alanine:D-alanine ligase (ddlB), partial cds; and cell division fts gene cluster, partial sequence.
AF492457

AF492457
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                       /gene="f
1662..2
                                                /translation="MGFNGAKKPKRATRGGIIAALDVGSTKVCCLIARVEDAGGVRIV
GIGHQIATGVRAGAIIDMEAAETSIGAAVHAAEDMANETIEDVIVNYSSPISHGENAE
VPVSGQEVTESDVRRALAHARSLQVGPDQALVHAIPVGFALDGSRGIRDFKGMYGERL
GVQAHVITSPAGAVRNLQTCVARCHLDIEGLVASPYASGLACLVDDEMEMGSACIDMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'translation-" KALLAPYGVRSPKGLVLTKGELTGGAHPMPAPYIVKPVDEGSTV
GVTLVREGONSPVGDAWTFGERALVEEFIPGRELTVGVLGGECRPLTVTEIRFEA
GVTDYDAKTSAGHAVHTVPAGLFEHVALEAKRLAVLAHRTLGCRGVSRSDFRWDDRKS
GTDGLFFLEINNQPGMTPLSLVPEQAASVGLTYGALVAWMVENAACQLD"
    GGTTTISVFSEGTLVWSDCIRLGGNHVTNDIARGLTTPVVHAERMKTLHGSAINSPAD
EREMIDVPQVGEEERLGANNLPKSYLVRIIQPRLEEIFEHVRSRLEHSGYAKLVGRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSTRLSIDPQFRPGFGGSANRGRDDRPVPPRAMAKSAQKGNRRR
AWPRWTRPAVKAAILLTPVLVVAGMAASAWQRGTIAETTAALQESLIQTSASAGFAIA
DVLVBGRTETDPASILRVLGVQRGDPILAVTLSDAKEKLESLPXVASXSIERHLPDIL
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/db_xref="GI:20136385"
/trans!a+io=="""
                                                                                                                                                                                                                                                                /note="may be involved in component of the septum; n
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PKILAALDNVPALREKVSAASWVGDRRWDLKLKNGVVVKLPEARMQSALRQLAEMDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="cell division
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/strain="Cd"
                                                                                                                                                                                                                 transl_table=11
                                                                                                                                                                                                                                                                                                              /gene="ftsA"
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                                                                                                                                                  GlyValLysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
                                                                                                                                                                                                                                                             AlaAspLysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGlu
                                                                                                                                                                                                                                                                                                              GAGCTGCAGCAGTATGTTGACACGCTGATCATCATCCCGAACCAGAACCTGTTCCGCATC
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3067. .>387"
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3 1353 c 1260 g 544 t 3 others
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1404 bp mRNA ] splendens FtsZ (MsFtsZ-mt) mRNA,
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Submitted (13-JAN-1999) School of
Grattan St. Parkville, Vic. 3052,
Location/Qualifiers
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Eukaryota; stramenopiles;
1 (bases 1 to 1404)
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Beech, P.L., Schultz, T.,
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                                                                                       ACTTGCTTGACTGAAAACAAGCTTCAGCTAGGAAAAGAGTCAACCCAAGGATTGGGTTGC
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/ftsnslation="mritganrilssrstriptsucytesycogogonavumiark
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/strain-"MUCC 294"
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56-1 Shilimdong Kwanaku, Seoul 151-742, Korea
Location/Qualifiers
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/transl_table=11
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DSJLLPK"
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502. .1530
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<1. .465
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/protein_id="AAD53917.1"
/db_xref="GI:5834351"
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                  /gene="kefC"
8520. 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5933. .7819)
/gene="zmllorf2"
complement(5933. .7819)
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/codon_start=1
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QPETDPRLPVSKGGVVZENVENKGLVDSIVQSTRGRHNAFAWIGVGDNSVMLARDPKD
RGMFGTWLGIKPWLRDKGIDIQSSMGGVETAFNARGGDRHGLTTAYQWLVQASFDMER
LGVVKGGKTENNEFCKAMTGCSFMSLGFCGNQAGNLVGDYWYNWPVSNWAGRVTYQVSKE
VTIGAGVFDVNRKNIQGKVLHENFYNDNPFHPEAGLYIGEVKWAPKFGRENNLEGLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPDEIFQYLEQAHRLAFGYSVIPWEXRYGMÄGGIVPVLLAAAMKMGDIMNTQSFLYWV LPHAITALLSLGVIWSAYKGELHSFTTGCLAMEVAATWYEJTLFTAHPLSESLSEAA FMPAAYVLIAEEKKKSSLILSGELMGLSALLROYJPSILFITLFTHRINVROWGYFI LGGLGAVFISSLSDIFIGESYPLLWLFKNIQONLIFHRAEDYGTAPIYSYFFDIWTNWK WFSLILPITPLHKKAQATAFTAWGACSFLCSTGNISHWYQYRGVIQAEMKARSLS LLIEJTPLHKKAQATAFTAMGACSFLCSTGNISHWYQYRGVIQAEMKARSLS LLIEGATITPLHKKAQATAFTAMGACSFLCSTGNISHWYQYRGVIQAEMKARSLS LLIEGATITYPLHKKAQATAFTAMGACSFLCSTGNISHWYQYRGVIQAEMKARSLS LLIEGATITYPLHKKAQATAFTAMGACSFLCSTGNISHWYQYRGVIQAEMKARSLS LLIGATIYQIDYWESGGYSLLHRPIPIYSLLPSNMYSTRYPDPIALSPSLFSASNAII
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LSSPSSEISSDRDLSLADDILEDDPDNESENLALFADFFIPGDAVKLKELVTELECRY
TTAALNSANNIVSDAARLLGLHRTTLIEKMNKYKISRS*
                                                                                                                                                                                                                 FDGWYTDDKSYNLRYYQDVAMQTGYSSQGPEVRGRYGAYVTAEQQVLRFDSHRQLTVA
FRALKNDGRTNKSTAEVSAYAILFGVSKERPDDWVGLGAGTTWLSNAFLKSQALSAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAASSGKNLPKEYRQVSCYPQKNGEKTEDICLFFRPSSCFKKETADNFEINKVLKNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="phosphatidylinositol glycan homolog"
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4117. .5646
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TGPSGSGKENVASSIHASSPRSQGFFIPVNCGAIPRDLLESELEGHEKGAFTGANGQT
TGPSGSGKENVASSIHASSPRSQGFFIPVNCGAIPRDLITSTGATRATIGATRATISATHR
GGREEEADAGTLFILEIGDNEPEMOVKLLRVLEDNITIRVGGRQSIHVDTRIISATHR
DIHNAIEHKAFREDLFYRLAVFPIHLPSLADRSDDVPLLAEYFCDRLPENRKFCFSSD
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LKGHTKDGFVFFTNLGSRKGHELLENPVATLLFHWKKLRRQVRIEGAATLISDEEADA
YFATTARKSQLGAWASEQSRPLPARDVFEKRIADIEARVEGKDVPRPPYWTGFRVSPI
/gene="kefC"
                                                                                                                                                                            RHQEYYSELFYNIQLSPAVFLRPNIQYVVHPGGYYARGPVDTPYNYNSKNIILLGLKS
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/protein_id="AAD53920.1"
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/protein_id="AAD53919.1"
/db_xref="GI:8834353"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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complement(13374..14303)
/gene="zmllorf3"
complement(13374..14303)
/gene="zmllorf3"
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DHLRAAGFLYADGVLPANEEGGYVLARIMRRAMRHAHLIGAKEPLMYRLVPALLSEMG
MAYPELVRAKALIEETLRLEETRFRQTLANGLKILKDETQHLKSGDTLPGAVAFRLYD
TYGFPYDLTADALFARNLYVDQAGFDAMAEORKAARAAWKGSGEKASDEIWFDIADQ
LGGTEFTGYTAEKGSGQIIALIKDGKRVETAKQGDDTTIITNQTPFYGESGGQKGDIG
VITGNNDLKMTVTDTQKPLGRIHAHLAKIEKGELKIGDDIQLYVDLNHRNRLRANHSA
THLLHAALRDJGGHYSQKGSMYSAERLFFDFSHQKALSDQELAAIEAEVNQQILNNS
VTTRLMTPESAVEAGAMALFGEKYGNEVNLSMGSCLMDQNEESSWSVELCGGTHVS
ALGQIGLFHIVSETAVSSGIRRIEAVTGEEARLUGGRRLLRETASIIKAVPEEVPT
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/gene="alas"
complement(10368. .13034)
/gene="alas"
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LFEDLALVPIIFALVPWHLMGKIIAGTDLIATINGGGATVLAILVLGAFALPTLFAQA
ARTKSARVFLSISLLVVLLASVATSAMGLSPJYGALTAGLLIAETDYNVEVLBWYILPF
QRLALGVFLLTVGMSLDLRLIMANWQALALGVAGVVLVKTLVTSTLLRLSHVRLATAV
ESCLLMSAPSETILVILATARQAQLLMPSTAAFWEIVTAIGLTITPHLAKISHRVSLK
LTLREHHLTLFSNREFIEDDQNHTIVAGIGRVGKVIAVVLTSEKRPYLAIDSSDLVI
NAKRDGYHATFGDISNPVFIQQLGNKINAVVLAINDPVSNVNVHRLHTIYPDLTIIA
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DPSHGDLAINAAMVLAKAAKTAPRALAEKLVESLSQLEGVESVEIAGPGFINIRLTDD
CWRKELTHILEQGQDYGRSDIGQNLKYNVEYVSANPTGPMHNGHCRGAVVGDALASLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDDKDQEHDAMNSHGRPQENNTYNRPFGRSNAHGSSRDDTSDFY
DHHSADADDGDEDDSLPWLEPVEDDDNGHGGNIFQIVIVALVALLTLALLGIGLYWWF
HRPPAVSGNASVITAEPGPYKTKPREPGGMKIEGEGESAYAASEGRDINSSIDTSVQP
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/protein_id="AAD53926.1"
/db_xref="GI:5834360"
                                                                                                                                                                                                                                                                                                                                                                                         complement(14307. .16049)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGVMSSLHNDAHPADEAKKAPAGCRCYPVGCLW"
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PAAPVKHEKEVKPAEHPVKAAEREKPPVAVVKPAAKVEKPEAEHQAEVAKPKSREDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="unknown"
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/db_xref="GI:5834359"
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LLGLIDENKKIIESGVIALITVNEGRASVAIGVSDSLKGKISAVDLVRKAVETLGGKG
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KERVIELAWGLITKEWGLDPERLCVTVYHTDEEAFNLWRKIAGLPEDRIIKIATSDNF
WSMGDTGPCGPCSEIFYDHGPEIPGASGLADEDGDRFVEIWNLVFWQYEQVNAETRLN
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/translation="MITTNEIRRSFSRIFRKEWPSDSTIAPLVPQNDPTLMFVNAGMV
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                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="argS"
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DFAGYKVTREYYVNDAGQQVQTLARSAYMRYREALGEEITIPEGLYPGDYLVPVGKLI

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Query Match:
                                    FEATURES
                                                   COMMENT
                                                                                                                                                                                                                                                                                         SOURCE
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                                                                                      JOURNAL
                                                                                                                                                                                        TITLE
                                                                                                                       AUTHORS
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               2 (bases 1 to 1542)
Lee,K.N., Massung,R.F., Padmalayam,I. and Baumstark,B.
Direct Submission
Submitted (07-JAN-2000) Centers for Disease Control and Prevention,
1600 Clifton Rd., Decatur, GA 30329, USA
On May 15, 2001 this sequence version replaced g1:12655827.
1. 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee,K.N., Massung,R.F., Padmalayam,I. and Baumstark,B. Characterization of the ftsZ gene in Ehrlichia chaffeensis, agent and Rickettsia rickettsii
                                                                                                                                                                                                                               Ehrlichia chaffeensis
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Anaplasmataceae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                          complete cds. AF221944
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Ehrlichia chaffeensis cell division
                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                           AF221944.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluLeuAlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAla 140
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                                                                                                                                                                                                                      (bases 1 to 1542)
 /organism-"Ehrlichia chaffeensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 SerLeuAlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGly 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                               AF221946 1540 bp 1
Rickettsia rickettsii cell division
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complete cds.
AF221946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaAspLysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGlu
                                                                                                                                                                                                                                                                                                                     ACAAAACCTTTCCACTTCGAAGGGGCACATCGAATGAGGACAGCAGAATTTGGGTTAGAA
                                                                                                                  GGTGTTCGTGGCATCACTGACTTAATGGTAATGCCAGGGCTCATTAATCTA
                                                                                                                                                                                 SerThrProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLys 121
                                                                                                                                                                                                                                                                                                                                                                                     GCTGCTCCTGTAATTGCCAGAGTTGCCAAAGGAGAACAAAATTTTAACCATAGGAGTTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArg
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/db_xref="G1:14043017"
/db_xref="G1:14043017"
/translation="MSLNICLPDQSLLRPRITVFGVGGAGGNAVNNMIQSNLHGVNFV
/translation="MSLNICLPDQSLLRPRITVFGVGGAGESINEIIEEISDSNML
FITAGMGGGTGTGAAPVIARVAKENKIITIGVVTKPFHFEGAHRNRTAEFGLEELQRY
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AIMSEMGKAMMGTGGAEGENRAIAAFKLADTVLHTGVRGITDLMVMPGLINLTGGLDMTL
AIMSEMGKAMMGTGGAEGENRAIAFKLADTVLHTGVRGITDLMVMPGLINLTGGLDMTL
EEVDAAANRIREETDSHANIIFGSTFKKESEGKIRVSVLATGIDNEEVVIQNKSALKD
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3 232 c 280 g 453 t
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/transl_table=10
/product="cell division protein
/_----in id="AAK00615.2"
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254. .1519
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AUTHORS
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                  101 ValSerThrProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyVal 120
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                                                                                                                                                                        321 TACCTAGAAAATAGCAATATGGTATTTATTACGGCAGGTATGGGCGGTGGTACAGGTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-JAN-2000) Centers for Disease Control and Prevention,
1600 Clifton Rd., Decatur, GA 30329, USA
On May 15, 2001 this sequence version replaced gi:12655831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agent and Rickettsia rickettsii
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                                                                                                GlyAlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyVal 100
                                                                                                                                                                                                                     MetLeuGlnAspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThr
                                                                                                                                                                                                                                                                             GGAGCTTCTCCTGAGGTTGGAGCACTTGCTGCTCAAGAATCAGAAAGCGAAATTCGTAAT
                                                                     GGTTCTGCACCGGTTATTGCACGCATTGCTAAAGAACTAGGCATCCTTACGGTTGGGGTA
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39. .1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-APR-2001) Unite des Rickettsies, Faculte de Medec: CNRS UMR 6020, Universite de la Mediterranee, 27 boulevard Jean Moulin, Marseille Cedex 05 13385, France A public version of R. conorii genome database is accessible at http://igs-server.cnrs-mrs.fr/. The database intends to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selfish DNA and the origin of genes science 291 (5502), 252-253 (2001)
3 (bases 1 to 8328)
0 Ogata, H., Audic, S., Renesto-Audiffren, P., Fournier, P.-E., Barbe, V., Samson, D., Roux, V., Cossart, P., Weissenbach, J., Claverie, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                      updated data. Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful Comments to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ogata, H., Audic, S., Renesto-Audiffren, P., Fournier, P.-E., Barbe, V., Samson, D., Roux, V., Cossart, P., Weissenbach, J., Claverie, J.-M. and
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Selfish DNA in protein-coding genes of Rickettsia Science 290 (5490), 347-350 (2000)
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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, Faculte de Medecine, 27 boulevard Jean

R. prowazekii

fever group.

BCT 14-SEP-2001 complete

Comments to the

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complement(3852. 3880)
/HOLE-"REP01, repeated element" complement(5424. .6668)
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FEVDNAANRIREEVDNLDANIIFGSTFNPELKGMIRVSVVATGIDADKVPTYKPAIAE
TTNIYPEETYNKAIAQPTQIEEMPDFNSYSTENIEITDSPINQNFIGNEKELGLHANT
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VDTLIVIPNQNLFRIANEQTTFADAFKMADDVLHAGVRGVTDLMIMPGLINLDFADIK
                                                        5303.
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/gene-"ampG2"
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GTAACTAAACCTTTCCATTTTGAAGGCGGTCATCGTATGAAAACTGCCGATAAAGGACTT
                              ValSerThrProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyVal 120
                                                                                                 GlyAlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyVal 100
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RERVILSFRKSNHRIMVATDVAARGLDIPHTQHVINYDLPMCPEDYLHRIGRTGRAGA
TGHALSFISPDDVIRWRAIDRLVNKGESTPRSEFRSDKNNRKRSFGKRAGGDGKKFNA
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ASSQTGSGKTLAYLLELIDSFIKNKTTALILVETELATQIHSTUKVTTSKINSAW
LIGGEPMPKQDIQLKKNPKVIIGTPGRIIDHLMRGSLKIDRIGITVLDEMDRMLDMAK
KEQLEEINKFLPEKRQVLMFSATMPKHIIAVSQKYLNNPVRITVGATNKAAAEIKQES
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7756. .7838
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/protein_id="AAL03558.1"
/db_xref="GI:15620136"
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1445 c 1263 q
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/gene="RCRNA30"
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/protein_1d="AAL0359.1"
/db_xref=ngi:15620137"
/tiansiation="MATNIVGKVKWYNSTKNFGFIEQDNGGKDVFVHKSAVDAAGLHS
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/note="RC1020"
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Ehrlichia sp.
complete cds.
AF221945
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Anaplasma phagocytophilum
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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Lee, K.N., Massung, R.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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     SerGlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArg
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/trans1_table=11
/product="cell division protein FtsZ"
/product="cell division protein FtsZ"
/protein_id="AAK00616.1"
/protein_id="AAK00616.1"
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FITAGMGGGTGTGAAPVIAKAAKDSKILTVGVVTRPFHFEGAHRMKTAEYGLEELQKH
VDTLLVINQNLERIANEENTFEADAFKLADTVLHFGVRGTILDLWYMFGLLNLDFADVK
TOTLLVINQNLERIANEENTFEADAFKLADTVLHFGVRGTILDLWYMFGLLNLDFADVK
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FEVDAAANRIREEVDEEANIIFGSTFDENSAGRIRVSVLATGIDSTHTSNPKGRMTRG
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/db_xref="taxon:948"
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                                                                                                                                                                                                                                                                      Submitted (26-MAY-1998) MCB, Harvard Cambridge, MA 02138, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium lentocellum Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                     Angert, E.R.
Direct Submission
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AF067822.1
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Clostridium lentocellum
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8
                                        REFERENCE
AUTHORS
                                                                                                           SOURCE
ORGANISM
                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                 RESULT 9
AE013119/c
                                                                                                                                              KEYWORDS
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                                                                                                                                                            AE013119 11683 bp
Thermoanaerobacter tengcongensis
the complete genome.
AE013119 AE008691
AE013119.1 GI:20516647
1 (bases 1 to 11683)
Bao,Q., Tian,Y., Li,W., Xu,Z., Xuan,Z., Hu,S., Chen,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong, Tan,H., Chen,R., Wang,J., Yu,J. and Yang,H.
                                                                                      Thermoanaerobacter tengcongensis
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales
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                                                                        Thermoanaerobacterlaceae; Thermoanaerobacter
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                                                                                                                                                                                                                                                                                                                                                                                                           LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATTTAGTTTTGAAGGTCGCAAAAGAATGATTAATGCAGAGAAAGGTATTGCAGAGCTT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu
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                    Dong, X.,
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                Dong, W., Yang, J.,
, X., Ma, Y., Ling, L
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AUTHORS
TITLE
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Direct Submission
Submitted (07-OCT-2001) Institute of Microbiology, of Sciences, Beijing 100080, China
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 11683)
Li,W., Xuan,Z., Yang,J., Ling,L. and
Direct Submission
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Direct Submission
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                                                                                                                       E-value 2.00E-82"
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complement(109. .1195)
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                                                                                                                                                                                                                                                                                                                                                            complement(1197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   score 95.9, E-value
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(AP001515) cell-division initiation protein (septum formation) (Bacillus halodurans), score 352, E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                .1195)
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.10E-25"
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                                                                 involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
/protein_id="AAM24844.1"
/db_xref="G1:20516654.1"
/db_xref="G1:20516651"
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GPGVIYTYNDSKQPVPPGQDPNLFLVHDEDLLRIVNELRAAGAEAISLNDQRLIATSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Best Blastp hit = gi|1075848|pir||C43727 conserved /note="Best Blastp hit = Best Blastp hit = Bacillus subtilis gi|1129091|gb|AAR83971.1| (M31827) ORF4; putative [Bacillus subtilis] gi|2633896|emb|CAB13398.1| (Z9911) similar to hypothetical proteins [Bacillus subtilis], score 126, E-value 2.00E-28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Pfam match to entry FtsA, Cell division protein FtsA, score 452.4, E-value 3.80E-132" complement(2433. .2437)
/gene="FtsA2"
                      complement(4291.
/gene="MurA2"
                                                                                                                    KIEIIGDGNAVFMQ"
complement(3562.
/gene="TTE1642"
                                                                                                                                                                                                                        /translation="mnkrafrviffllilavlsyvfafhtnyfkiksikvvgnqilsy
ndikeiskiqagtnifkvnpkqveknllenpyikeckvkilypnrveifveerrvvaq
vryksdylkidkegvivekgsftpgllliegikveryqigkklngnfdktllsevlgl
                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3536. .4234)
/gene="FtsQ"
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/gene="TTE1642"
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/gene="TTE1642"
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GIRASFEEKFDNLIFITGFFGNIILAGGLAYIGDVLGVPIYLAAVFVFGSRLFSNFAY
IRRYLIDRMRRR"
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(AP001515) small basic protein [Bacillus halodurans],
score 100, E-value 5.00E-21"
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/gene="FtsA2"
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SVTALQNMEKCVRKAGLEIDGIIVGPLATSEAVLLKDERELGYALIDVGAGVTDISVF
KNGGLIYSSMIAVGGWHITNDLSVGLKISFEBAENIKKKYGTLEKVDDPRLEPIKIAS
LAGKSKTTTDINEIADIIEARVSELLTLYYERLEEAGVLEDIVTNVVITGGGISFLKG
                                                                       /gene="FtsQ"
                                                                                                                                                                                                                                                                                               /product="Cell division septal protein"
/protein_id="AAM24845.1"
/db_xref="GI:20516652"
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/gene="TTE1641"
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/protein_id="AAM24843.1"
/db_xref="GI:20516650"
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/gene="TTE1641"
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/gene="TTE1641"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="FtsQ"
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US-09-770-509-2 (1-178) x AE013119 (1-11683)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu
                                                                                                                         84 ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
                                                                                                                                                                                                                                                                                                                                                                                   {\tt 44\ ProGluLeuGlyLysArgSerAlaGluGlnLysValAspIleGlnArgMetLeuGln}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu ::::::|||||||||||||||
                                                                                                                                                                                                                            CCTGAAATTGGTAAAAAAGCGGCAGAAGAGTCGAGGGAAGAGATCGAAAGAGCGATAAAA
                                                                 CCAGTTGTAGCTGAAATTGCAAAGGAACTTGGTATTTTAACTGTAGGCGTTGTGACTAAA
                                                                                                                                                                                           GGTGCTGACATGATATTCATAACAGCGGGCATGGGAAGGCGCACAGGTACAGGAGCAGCT
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/db_xref="GI:20516653"
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ARNKKAPISFPGGCDIGHREPIDLHLKGLKKLGVEIEESYGYIRCKGVRVRGMEIHLDL
ASVKAAPISFPGGCDIGHREPIDLHLKGLKKLGVEIEESYGYIRCKGVRVRGMEIHLDL
PSVGATENIIMLAATLADGITVIRNAAKEPEIEDLQNETKEHLEPLISKLKETGGELKTG
KKLHDTEXTIIPDRIVAGTYLCAAAMTRGELTYVKALKEHLEPLISKLKETGGELKTG
KKLHDTEXTIIPDRIVAGTYLCAAAMTRGELTYVKALKEHLEPLISKLKETGGELKTG
KUNDYIKITCNKRPKAVDMIVTLPYPGFPTDLQPQIVSVLGIAEGTSIVTETIDNRFKY
NDYIKITCNKRPKAVDMIVTLPYPGFPTDLQPQIVSVLGIAEGTSIVTETIDNRFKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry EPSP_syntase, EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase), score 407.8, E-value 1.00E-118" complement(5552. .5556)
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(AP001515) UDP-N-acetylglucosamine-N-acetylmuramyl-
(pentapeptide)pyrophos [Bacillus halodurans], score 306
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EHIDRGYESLEKALKSVGADIVRIM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 279110)
Andersson, S.G., Zomorodipour, A., Andersson, J.O.,
Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K.,
Eriksson, A.S., Winkler, H.H. and Kurland, C.G.
Eriksson, A.S., Winkler, H.H. and Furland, C.G.
The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia prowazekii.
Rickettsia prowazekii
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2 Andersson, S.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ235272.1 GI:3861033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPXX03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ235272 AJ235269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGGAATTTCTGATTTAATAGCTGTCCCGGGGCTTGTGAATGTG 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAGACATCTATGCTAGATGCTTTTAAGCTGGCAGATGACGTTTTAAGGCAGGGCGTT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAGTACGTAGATCCATAACGATCCCTAATGATAGATTATTACAGGTAGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTTCACTTTTGAAGGAAGGAAGAGATGGCGCAGGCAGAGATGGGGAATAGAAGATTTA
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prowazekii strain Madrid
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.3091
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Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                          misc_RNA
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I SNNVARLANTTL I TVDNTDAQVKL I GFDLRNI CVSSGSACSSGK I SKSHVLT NMG I R
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                                                                                                                                                                                                                                                                                           .10893)
     Length:
                                                                                            PRECURSOR (ppdK)."
                                                                                                                                                     REFERENCE
AUTHORS
TITLE
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AUTHORS
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                                                                                                      Direct Submission
Direct Submission
Submitted (28-SEP-1995) Maria Navajas,
Submitted (28-SEP-1995) Maria Navajas,
                                                                                                                                                                                                                                            Tsagkarakou,A., Guillemaud,T., Rousset,F. and Navajas,M. Molecular identification of a Wolbachia endosymbiont in a Tetranychus urticae strain (Acari: Tetranychidae)
Insect Mol. Biol. 5 (3), 217-221 (1996)
                                                                                                                                                                     Navajas, M., Tsagkarakou, A., Guillemaud, T. and Rousset, F.
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                                                                                                                                                                                         (bases 1 to 697)
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/db_xref="taxon:956"
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Rickettsiales;

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                                                                                                                                                                                                                                                                                                                                         GTGCGACGTATGCGCATTGCAGAGCTTGGACTTGAAGAGTTGCAAAAATACGTAGATACA
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NEKTTXVDAFQLADNVLHIGIRGVTDLMIMPGLINLDFADIETVMSEMGKAMIGTGEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jager, C.R., Pintureau, B. and Heddi, A. Comparison between phylogenetic trees of and their Wolbachia endosymbionts Russ. Entomol. J. 7 (3-4), 163-168 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolbachia sp. 123B.
Wolbachia sp. 123B.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Wolbachieae; Wolbachia.
1 (bases 1 to 868)
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2 (bases 1 to 868)
                                                 -----GlyIleLeuThrValGlyValValSerThrProPheArgSerGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=2
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SDAEKALSNPLLDNVSMKGAQGILINITGGGDMTLFEVDAAANRVREEVDENANIIF
SDAEKALSNPLLDNVSMKGAQGILINITGGGDMTLFEVDAAANRVREEVDENANIIF
GATFDQAMEGRVR"
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<1. >868
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1 (bases 1 to 868)
Jager, C.R., Pintureau, B. and Heddi, A.
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Proteobacteria; alpha subdivision;
aceae; Wolbachieae; Wolbachia.
/transl_table=11
/product="cell d
                                                                                             /gene="ftsZ"
<1. .>868
                                                                                                                                                         /specific_host="Trichogramma cordubensis"
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                                                                                                                                                                                                              /strain="1032"
                                                /codon_start=2
                                                                     /gene="ftsz"
                                                                                                                                                                                                                                  /organism="Wolbachia sp.
                                                                                                                                                                                                                                                                             Location/Qualifiers
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    division
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    Fts2
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RESULT 15
WSU95750
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                                                                   KEYWORDS
                                                                                                                                DEFINITION
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Wolbachia sp. 1148.
Wolbachia sp. 1148
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
                                                                                                                     WSU95750 868 bp DNA linear BCT 11-AUG-199 Wolbachia sp. 1148 cell division protein Fts2 (fts2) gene, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GlyIleLeuThrValGlyValValSerThrProPheArgSerGluGly 109
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                                                                                                                                                                                                                                                                                                                                                                                        GTGCGACGTATGCGCACTGCAGAGCTTGGACTTGAAGAGTTGCAAAAAATACGTAGATACA 424
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                                                                                  GI:2078544
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/db_xref="GI:2078543"
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LeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSerThrThrMetLeu

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US-09-770-509-2 (1-178) x WSU95750 (1-868)
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Query Match:
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Jager, C.R., Pintureau, B. and Heddi, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-MAR-1997) Laboratoire de Biologie AppinSA-Lyon, 20, av A. Einstein, Villeurbanne 69621,
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                                                                                                                                                                                                                                                                                                      LeuGlnAspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGly 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLeuAlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGly 41
GTGCGACGTATGCGCACTGCAGAGCTTGGACTTGAAGAGTTGCAAAAATACGTAGATACA
                                                                                                                                                                                                                                                                              ATAAGGGACAGCCATATGCTCTTTATCACAGCAGGGATGGGTGGTGGTACTGGAACAGGT 244
                                                                                                                                                                                                                                                                                                                                                                         GCTTTGCCTGATATTGGTAAAGGTGCAGCAGAAGAATCAATTGATGAAATTATGGAGCAT 184
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                                    ProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLysTyrValAspThr
                                                                                        GCAAAAGAAAAAAAGATACTGACTGTTGGAGTTGTAACTAAGCCGTTCGGTTTTGAAGGT
                                                                                                                                    -----GlyILeLeuThrValGlyValValSerThrProPheArgSerGluGly
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/db_xref="taxon:59579"
<1. .>868
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GATFDQVMEGRVR"
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Search completed: June 2, 2003, 09:39:19 Job time: 2508 secs
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Command line parameters:

MODEL-frame+_P2n.model -DEV-xlh
-Q-/cgn2_1/USBTO_spool_UE09770509/runat_27052003_083647_18810/app_query.fasta_1.327
-Q-/cgn2_1/USBTO_spool_UE09770509/runat_27052003_083647_18810/app_query.fasta_1.327
-DB=N_Geneseq_101002 -QFMT-fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09770509_eCGN_11_1263_erunat_27052003_083647_18810 -NCPU=6 -ICPU=3
-NO_MAMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSBADCOK=100 -LONGLOG
-NO_MINCHAN - NAMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSBADCOK=100 -LONGLOG
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Maximum Match 100%
Listing first 45 summaries
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WO200228891-A2.		Listeria innocua.		infection; ds.	Antibacterial; Listeria; food contamination; mutational analysis;		Listeria innocua contig DNA sequence #6.		29-AUG-2002 (first entry)		ABQ67193;		ABQ67193 standard; DNA; 213251 BP.	ABQ67193	RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 213251 BP; 70939 A; 36026 C; 43257 G; 63029 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating infections by Listeria, and are useful as immunogens in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
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                                   AAAGAAGCGGTGGATACTTTAATTGTTATCCCTAACGACCGTTTACTTCAAATTGTTGAT
           LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                       AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
                                                                                   CCATTTGGTTTTGAAGGACCAAAACGTACGAAACAAGCCCTAACTGGAACAGAAGCAATG
                                                                                                         ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu 123
                                                                                                                                  CCTGTTATCGCTCAAATCGCAAAAGAAATGGGCGCTCTAACTGTCGGTGTTGTTACACGA 170456
                                                                                                                                                 ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
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                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the genome sequence of Listeria monocytogenes BGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence for Listeria monocytogenes, useful e.g. for treation of Listeria and related bacterial infections, and
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                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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RESULT 3
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  New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ69245;
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                                                                                WPI; 2002-332479/37.
                                                                                                                                   Kunst F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria innocua DNA sequence #684.
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                                                                                                                                   Glaser P;
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                             13-AUG-2002
                                                                                ABK77373;
                                                                                                                             ABK77373 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3011208 BP; 941651 A; 568176 C; 559189 G; 942192 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of monitoring differential expression of CC genes in a first Bacillus cell relative to expression of the genes in CC other Bacillus cells, comprising hybridising labelled nucleic acid probes CC isolated from Bacillus cells to a substrate containing array of Bacillus CC genomic sequenced tags (GST), examining the array, and determining CC relative gene expression by an observed hybridisation reporter signal of CC aspot in the array. The method is useful for measuring the expression of GC genes in a first Bacillus cell relative to expression of the same genes CC in one or more second Bacillus cells. The method is useful for monitoring GC global expression of several genes from a Bacillus cell, discovering new GC genes, identifying possible functions of unknown open reading frames and CC monitoring gene copy number variation and stability. Monitoring changes CC in expression of genes may be used to provide a representation of the way CC environmental stress or other physiological provocation. Extensive GC environmental stress or other physiological provocation. Extensive GC equals one gene or one open reading frame, since sequence information is considered of the invention. This sequence represents a genomic sequence tag (GST) used in the content of the invention of the provention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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27-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO)
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                                                                                           103
  11; SEQ ID NO 4664; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVOZYMES BIOTECH INC
                                                                                                                      LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu
                                                                                     CTGCAAGGTGTTGATTTATTGCAGTCAATACAGATGCACAAGCACTCCATTTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         950 BP; 277 A; 184 C;
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Conservative:
Mismatches:
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22-JUL-1997;
22-JUL-1997;
  AAX20248
Borrelia
                                                                                                                                                                                                                                                                                                                   Clayton R, White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                  Claim 1; Page 738-800; 1128pp; English.
                                                                                                                                                                     New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention
                                                                                                                                                                                                                                                              WPI; 1999-081217/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX20250;
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                                                                                                                                                                                                                                                                                                                                                                                                      (MEDI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                ( HUMA - )
                                                                                                                                          therapy of infections, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GCGGAAAAGAAGTTGCAACTTGGCGGCAAACTTACTCGCGGCCTTGGCGCTGGCGCCAAC 22
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN GENOME SCI INC
  to \hbox{AAX}20402 represent polynucleotide sequences burgdorferi (Bb). Products derived from Bb can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGGCATTTCCGATTTAATTGCCACGCCTGGGTTGATCAACCTT
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97US-0053344.
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                                                                                                                                                                                                                                                                                                                                              Lathigra
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrella causes epidemic and
                                Borrelia burgdorferi
                                                                        Borrelia burgdorferi; spirochete; bacterium; pathocepidemic relapsing fever; endemic relapsing fever;
                                                                                                                       Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                      04-MAY-1999
                                                                                                                                                                                    AAX20248;
                                                                                                                                                                                                                 AAX20248 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                              infection;
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                                                                                                                                                                                                                                                                                                                                       ACCATTAAAGATGCTTTTAAGCGTGCAGATGATGTTCTTAGAATGGGCGTTCAAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                               GTAGATACATTGATCATTATTCCAAATCAAAAGCTTTTAACTGTTGATGACAAAAGAACC
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                                                           elapsing tever; endemic relapsing fever; Lyme diagnosis; characterisation; detection; ds.
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                                                                                                                        #1.
                                                                           pathogen; Lyme disease;
fever; Lyme borreliosis;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 910715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 157-671; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, p
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                                                             SerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLysTyr
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                                                                                                                                   AlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThrProPheArg
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97US-0053377.
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                                                                                                            The invention describes a method of monitoring differential expression of CC genes in a first Bacillus cell relative to expression of the genes in CC other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus CC genomic sequenced tags (GST), examining the array, and determining CC relative gene expression by an observed hybridisation reporter signal of CC a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes CC in one or more second Bacillus cells. The method is useful for monitoring CC global expression of several genes from a Bacillus cell discovering new CC genes, identifying possible functions of unknown open reading frames and CC monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way CC in which Bacillus cells adapt to changes in culture conditions, CC environmental stress or other physiological provocation. Extensive collow-up characterisation is unnecessary, when one spot on an array cequals one gene or one open reading frame, since sequence information is the content of the invention of the invention is sequence represents a genomic sequence tag (GST) used in the content of the invention is a genomic sequence tag (GST) used in
                                                        Note: The sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 180; 200pp; English.
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27-MAR-2001;
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21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                     Antisense; cantibiotic;
                                                                                                           21-MAR-2001;
                                                                                                                                                                                                                    Enterococcus faecalis
                                                                                                                                               27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the
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AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
                                                                                                                                                                       ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
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                                              CCATTTAGTTTTGAAGGTCCAAAACGTGGTCGTTTTTGCCGCTGAAGGAATTGCCTTATTA
                                                                                           ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu 123
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                         The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the GC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumonlae, Pseudomonas aeruginosa and Enterococcus faecalis: The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation of the printed specification, but was obtained in electronic format directly from WIPD at
                                                                                                                                                                                                                                                                                                                                                            Claim 27; Seq ID No 3854; 511pp; English.
              ftp.wipo.int/pub/published_pct_sequences
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23-MAY-2000;
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and focuse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 767-783; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A computer readable medium has been developed which has recorded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No . :
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                                                                                               27611 AAAGAAAACGTTGATACACTATTAATTATCTCAAATAACCGCTTATTAGAAGTCGTTGAC
                                                                                                                                                               27671
                                                                                                                                                                                                                             27731 CCAGTAGTTGCAAAAATCGCTAAAGAATTAGGCGCTTTAACAGTTGGTGATAACTCGT
                                                                                                                                                                                                                                                                                               27791
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                                                                                                                                                                                                                                              84 ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr
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LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu
                                 AAGAAAACGCCAATGCTTGAAGCATTTAGAGAAGCTGATAATGTATTACGTCAAGGTGTT
                                                                                                              CCATTTAGTTTTGAAGGTCCAAAACGTGGTCGTTTGCNTGCTGAAGGAATTGCCTTATTA
                                                                                                                                                                                ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu
                                                                                                                                                                                                                                                                                             GGCGCGGATATGATTTCATTACTGCTGGTATGGGTGGCGGAACTGGTACAGGTGCTGCG
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the blosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent woold for the production of production of yogurt and cheese.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 2365589 BP; 765914 A; 415261 C;
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                                                                                                                                                                      ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln 63
                                                                                            GCAGATACAGTTATTCAACTTGGGCCAAAATTGACTCGCGGTTTGGGTGCTGCTGCGCAA 1938703
AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyThrCysThrGlyAlaAla
                             CCTGAAGTTGGTAAGCGCGCAGCTGAAGAATCAGCTGAAACAGTATCACAAGCCCTTGAA
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This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81996 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                         Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1999; 99US-0165086
12-NOV-1999; 99US-0165124
01-FEB-2000; 2000US-0179531
                                                                                                                                                                                                                                                                   Disclosure; Page 97; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eisenberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drug target; growth; organism viability; characterisation; ds.
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             24-JUN-1998;
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                                                                                                           ium tuberculosis; strain H37Rv; strain CDC 1551; genome;
epidemiology; patient treatment; epidemic monitoring; ds.
                                                                                                                                                             (first entry)
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             98US-0103840
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           164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu
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Evaluating strain variation of Mycobacterium tuberculosis, comprise determining the nucleotide sequence of the strain at positions in tigenome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
3pp + Sequence Listing; English
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1. The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic 757371 Τ, 189 other

4 LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu GCCGCGGTATCGCTGATGGATGCTTTCCGTAGCGCCGACGAGGTGCTGCTCAACGGCGTG AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu CCCGTCGTCGCCAGCATCGCCCGCAAGCTGGGCCGCTTGACCGTCGGTGTGGTCACCCGG ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln CTCAAAGGCGTGGAATTCATCGCGATCAACACCGACGCCCAGGCGTTGTTGATGAGCGAT LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal CGGGAGAGTTGCGACACCCTCATCGTGATTCCCAACGACCGGTTGCTGCAGATGGGAGAT CCGTTCTCGTTCGAGGGCAAGCGACGCAATCAGGCCGAAAATGGCATCGCGGCGCTG AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla CCGGAGGTCGGCCGTAAGGCCGCCGAGGACGCCAAGGACGAGATCGAAGAGCTGCTGCGC AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 163 123 103 143 63 43 2407668 2407788 2407848 83 2407908 2408028 23 2407608

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ID AAI99682 standard;
                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in th genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                                                                                                                                                                       Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     at segdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                                                                                                                                                                                                                                      specification,
                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis genetics, epidemiology, patient treatment and epidemic
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        ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln
                                       GCCGACGTCAAACTCGACGTCGGCCGCGACTCCACCCGCGGCTGGGCGCCGGCGCGCCGAT 2409310
                                                       AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
                                                                                                 CTCAAAGGCGTGGAATTCATCGCGATCAACACCGACGCCCAGGCGTTGTTGATGAGCGAT 2409370
                                                                                                                     LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essentiagenes themselves and the encoded proteins. The prokaryotes used are
                                                                               Claim 27; Seq ID No 4715; 511pp; English.
                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                             WPI; 2001-611495/70.
P-PSDB; AAU34274.
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The pneumoniae is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
583 CAAGGTATCTCAGACTTAATCGCTGTTTCTGGTGAAGTAAACTTA 627
                   164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
                                                              144 LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                                                                                                                124 AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeùAlaAsp 143
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Search completed: June 2, 2003, 14:34:50 Job time: 20511 secs

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Minimum DB
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-Q-/cgn2_1/USBTQ_spool/US09770509/runat_27052003_083650_18840/app_guery.fasta_1.327
-DB-Issued_Patents_NA -QFMT-fastap -SUFFIX-rni -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN+0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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1: /cgn2_6/ptodata/]

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3: /cgn2_6/ptodata/]

4: /cgn2_6/ptodata/]

5: /cgn2_6/ptodata/]

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US-08-987-146-3

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## ALIGNMENTS

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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-103-840A-2/c
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103840A Patent No. 6294328
  OTHER INFORMATION:
OTHER INFORMATION:
                                                                    ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                 LENGTH: 4403765
TYPE: DNA
: CDC 1551
: "n" bases at v
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various positions throughout the sequence \mathsf{t}, \mathsf{c} or \mathsf{g}
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Percent Similarity: Best Local Similarity:

1.02e-46 485.00 74.29% 54.29% 54.80%

Conservative: Mismatches: Indels:

4403765 95 35 45 0

Length: Matches:

Score:

Pred. No.: Alignment Scores: US-09-103-840A-2

Query Match:

US-09-770-509-2 (1-178) x US-09-103-840A-2 (1-4403765)

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ADDRICANT: FRASER, CWen R.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 7
LENCETT. 1
                                                                                                                                                                                                                                                                                                       ; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                    US-09-770-509-2 (1-178) x US-09-103-840A-1 (1-4411529)
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; ORGANISM: Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR ETILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1185
                                                                                                                                                                                                                                                                                                                                                 No.
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                                           163
                                                                                                                       124 AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
                                                                24 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
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{\tt ProGluLeuGlyLysArgSerAlaGluGlnLysValAspIleGlnArgMetLeuGln}
                                         GCTGAATCAAAAATTCAAATTGGTGAGAAATTAACACGTGGATTAGGTGCTGGTGCTAAT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGGCATCACCGACCTGATTACCACCCCGGGTCTAATCAACGTC
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73.148
54.298
54.248
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Patent No. 6350866
GENERAL INFORMATION:
                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: x-11
TELECOMMUNICATION INFORMATION:
                                                                                                      TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1005 base pairs
                                               STRANDEDNESS:
TOPOLOGY: 11nd
MOLECULE TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/987,146
FILING DATE: December 8, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ROCKĖY, Pamela K.
APPLICANT: Wang, Q. May
APPLICANT: ROSTECK JT., Paul R.
TITLE OF INVENTION: Streptococc
TITLE OF INVENTION: FtsZ
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: El1 Lil
STREET: Lilly Corp
CITY: Indianapolis
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                          TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
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Peery, Robert B.
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                                                                                                                                                                                                                                                                                                                        Sequence
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICATION NUMBER:
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US-09-770-509-2 (1-178) x US-08-987-146-3 (1-1005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6350866
GENERAL INFORMATION:
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                  SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence TITLE OF INVENTION: FtsZ
                                                                                                                                                                         STREET: Lilly Corpor
CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 ValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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Wang, Q. May
Rosteck Jr., Paul R.
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72.83%
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53.33%
US/08/987,146
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Conservative:
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FILING DATE: DOCUMENT OF THE CLASSIFICATION:

December 8,

Fueyo, Joanna Lynn

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US-09-770-509-2 (1-178) x US-08-987-146-1 (1-1008)
      Sequence 1, Application US/09120426 Patent No. 6197300 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                          592 ATTACCGATTTGATTACCAATCCAGGATTGATTAACCTT 630
                                                                                                                                                            166 ValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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                                                                                                                                                                                                                                                                                                  TyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSer 145
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                  Sequence 4, Application U
Patent No. 6350866
GENERAL INFORMATION:
APPLICANT: Skatrud, P
APPLICANT: Peery, Rob
APPLICANT: Rockey, Pa
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US-08-987-146-4
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CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 60/055,720
EARLIER FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Lonetto, Michael
APPLICANT: Pearce, Kenneth
TITLE OF INVENTION: fts2
FILE REFERENCE: GM10068
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ORGANISM: Streptococcus
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Peery, Robert B.
Rockey, Pamela K.
Wang, Q. May
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Query Match:

Percent Similarity: Best Local Similarity:

Alignment Scores:

Pred. No.:

; NAME/KEY: ; LOCATION: US-08-987-146-1

CDS 1..1005

FEATURE: ANTI-SENSE: MOLECULE TYPE: DI HYPOTHETICAL: NO

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TOPOLOGY:

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STRANDEDNESS: single

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US-09-120-426-1

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APPLICATION NUMBER: US/08/
FILING DATE: December 8, 1
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
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LENGTH: 2702 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
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STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
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OPERATING SYSTEM: PC-DOS/MS-DOS
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126 TyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSer 145
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Lilly Corporate Center
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Query Match:
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                                                                                                                                                                                                                               US-09-770-509-2 (1-178) x US-08-961-527-36 (1-21706)
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US-08-961-527-36
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                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-08-501
Sequence 36, App. No. 64201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                           2821 ACTGTTATTCAGTTGGGACCTAAATTGACTCGTGGTTTGGGTGCAGGAGGTCAACCTGAG 288(
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                                     46 LeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGlnAspSer 65
                                                                                                                                                                         6 GlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeuAlaPro 25
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pedness: double
                                                                                               H1sLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLysProGlu 45
                                                                                                                                                   GGCGTAGAATTTATCGCAGCAAACACAGATGTACAAGCATTGAGTAGTACAAAAGCTGAG 2820
GTTGGTCGTAAAGCCGCTGAAGAAAGCGAAGAAACACTGACGGAAGCTATTAGTGGTGCC 2940
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72.83%
52.60%
53.33%
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US-09-381-862-4
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                                                                                                                                       APPLICATION
FILING DATE: 23-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: CawLey, Jr., Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 1903(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10474-6300
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                                                                                                                    TELEFAX: (312) 474-04 INFORMATION FOR SEQ ID NO:
                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7143 base pair
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1997-71077
FILING DATE: 25-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP98/0128:
  MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ueyama, Hiroshi
APPLICANT: Abe, Kanako
APPLICANT: Keshi, Hiroyuki
APPLICANT: Matsuhisa, Akio
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                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 233 SC
CITY: Chicago
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                                                    nucleic acid
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  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLys 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Illinois
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                      linear
DNA (genomic)
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptococcus pyogenes ; STRAIN: Clinical Isolate SP-26-36 US-09-381-862-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08883515 Patent No. 5981836 GENERAL INFORMATION:
              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                STREET: 1 Sout
CITY: Madison
                                                                                                                                                                                                    ADDRESSEE: Quaries a Line street street: 1 South Pinckney Street
                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                        COUNTRY:
APPLICATION NUMBER:
                                                                                                                                       ZIP:
                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4153 ATAACCGACTTAATTACTAGTCCTGGCCTTATCAATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 ValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 TyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSer 145
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VENTION: PLANT CHLOROPLAST DIVISION GENES
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US/08/883,515
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RESULT 11
US-08-883-515-1
; GENERAL INFORMATION:
; APPLICANT: Austin-F
; APPLICANT: Burgess;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1628 base pairs
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NAME: Seay, NICHOLAS J.
NAME: SEAY, NICHOLAS J.
REGISTRATION UNWABER: 27,386
REFERENCE/DOCKET NUMBER: 9209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEPHONE: 608-251-9166
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       APPLICANT:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                              777 CGTCAGGGGGTTCGTGGGATATCTGATATCATTACGATTCCTGGTTTTGGTGAATGTG 833
                                                                                                                                                                                                                         140 AlaLeuAlaAspLysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeu 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 TCTCCTGTTTTGCCTGATAATAGGTTACAAATTGGTAAGGAGTTGACTAGGGGTTTAGGT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ThrGlyAlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGly 99
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                                                                                                                                                                                                                                                                                                                                                                                  ValValSerThrProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGly 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArg 21
                                                                                                                                                                                                  ACAGCTGTCTCAGTCTACTCCGGTAACAGAAGCATTTAATCTAGCTGATGATATACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGCATCTCTCAGAGACAATGTTGACACTCTCATCGTCATTCCAAATGACAAGTTGCTT 716
                                                                                                                                                                                                                                                                                                                                                 ATTGCCACAACGCCTTTCTCGTTTGAGGGTCGAAGAAGAACTGTTCAGGCTCAAGAAGGG 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgMetLeuGlnAspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyThrCys 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGAAATGTCAGGTGTGGAGTTCTGGATTGTCAACACTGATATCCAGGCTATGAGAATG 356
                     Austin-Phillips, Sa
Burgess, Richard R.
Burgess, Richar
German, Thomas
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Conservative:
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US-08-883-515-1
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                                                                                                                                                                                    TELEFAX: 608-251-9166 INFORMATION FOR SEQ ID NO:
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ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 920
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,718
FILING DATE: 17-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ziegelhoffer, Thomas L.
TITLE OF INVENTION: Transgenic Plants as an Alternative
TITLE OF INVENTION: Source of Lignocellulosic-Degrading Enzymes
                                                         FEATURE:
                                                                            MOLECULE TYPE:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pair
                                                                                                                                                                                                                           TELEPHONE: 608-251-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 831-2100
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                    TELEPHONE: 608-251-9166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                        NAME/KEY:
                                                                                            TOPOLOGY:
                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                               nucleic acid
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Y: U.S.A.
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                                                                                                                                                  1425 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osteryoung, Katherine W
WENTION: PLANT CHLOROPLAST DIVISION GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                        linear
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                                                                                                               double
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Alignment Scores: Pred. No.:

8.68e-45

Length:

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1996
LENGTH: 396
       Query Match:
DB:
                                        Best Local Similarity:
                                                                                                                                                ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1996
                                                        Percent Similarity:
                                                                            Score
                                                                                                           Alignment Scores:
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US-09-134-001C-1996/c
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6380370
GENERAL THEORY.
                                                                                           No . .
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                    6.68e-39
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55.38%
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                  Indels:
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6444799
GENERAL INFORMATION:
            FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
                                                                                                                                   APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                        PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
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                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-JAN
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/O FILING DATE: 23-DEC-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORKLOUN CORRECT: 755 PAGE MILL ROAD
TELEPHONE:
                                                                                                                     APPLICATION NUMBER:
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N: P. GINGIVALIS NUCLEOTIDES
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Sequence 3, Application US/09120426
Patent NO. 6197300
GENERAL INFORMATION:
APPLICANT: Fueyo, Joanna Lynn
APPLICANT: Lonetto, Michael A.
APPLICANT: Lonetto, Michael A.
APPLICANT: Pagarce, Kenneth
TITLE OF INVENTION: fts2
FILE REFERENCE: GM10068
CURRENT APPLICATION NUMBER: US/09/120,426
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 60/055,720
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Best Local Similarity:
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LENGTH: 665 base pairs
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LOCATION: 1...665
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                               ATCATATACAAAGATCTTAAGCTCGACAATGCTTTTGCCAAGGCAGACGAGACACTG
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                                                                                                                                                                                                                                                                                                                                     GAGGAAATGCGCAAAAAACGTAGATGCCTTGCTCGTGGTCAATAATGAACGG----CTCCGC
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; LOCATION: (1)...(669)
US-09-120-426-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 123, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                     COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
                ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                  FILING DATE:
                                                                                                                                      FILING DATE:
                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               ZIP: 20850
                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                CITY:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 GlyValLysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 AlaAspLysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGlu 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GluLeuAlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CAACTTCGTGAGCATGTAGACACTCTATTGATTATCTCAAACAACAATTTGCTTGAAATT 180
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53.61%
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PB340P2
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Indels:
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Matches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-123
                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: June 2, 2003, 14:09:19 Job time: 14522 secs
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                                       105 PheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAla 124
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196.00
70.27%
51.35%
22.15%
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38
14
22
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Command line parameters:

-MODEL-frame+_P2n.model -DEV-x1h
-Q-/cgp2_1/USBTQ_spool/US09770509/runat_27052003_083654_19004/app_guery.fasta_1.327
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALICN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US09770509_@CGN_11_1138_@runat_27052003_083654_19004
-NCFU=6 -ICPU=3 -NO_XLPXY -NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT
-DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10
-XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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          18
No. 1s the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.
                                                                                                    US-09-770-509-2
885
1 ASQLEGVEFIVAN
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Sequence 3854, Ap Sequence 128, Appl Sequence 9, Appl1 Sequence 32, App Sequence 32, App Sequence 3260, Ap Sequence 2360, Ap Sequence 2360, Ap Sequence 2360, Ap Sequence 1, Appl1 Sequence 1, Appl1 Sequence 20, Appl1 Sequence 20, Appl1 Sequence 536, Ap Sequence 1875, Ap Sequence 202, Appl1 Sequence 1876, Ap Sequence 202, Appl1 Sequence 202, Appl1 Sequence 202, Appl1 Sequence 202, Appl1 Sequence 204, App Sequence 7456, Ap Sequence 7456, Ap Sequence 7456, Ap Sequence 745, App Sequence 3, Appl1 Sequence 3, Appl1 Sequence 3, Appl1 Sequence 1038, App Sequence 3504, Ap Sequence 3504, Ap Sequence 3504, Ap Sequence 3514, App Sequence 3514, App Sequence 3514, App Sequence 3514, Ap Sequence 3514, App Sequence 3514, Ap Sequence 3514, Ap Sequence 3514, App Sequence 3504, Ap Sequen	

## ALIGNMENTS

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Sequence 1, Application US/09770509
Publication No. US20030082657A1
GENERAL INFORMATION:
APPLICANT: Kategiri, F.
TITLE OF INVENTION: OOMYCETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES
FILE REFERENCE: NADII.018A
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(535)
US-09-770-509-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-770-509-1
                                                                    Pred.
                                                                                  Alignment Scores:
                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 535
TYPE: DNA
                                                                                                                                                                               ORGANISM: Phytophthora infestans
                                                                  No::
2.03e-107
885.00
100.00%
100.00%
100.00%
                                                 Length:
Matches:
               Conservative:
Mismatches:
 Indels:
 535
178
0
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Result

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Score

Match

Length

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509 502 495

100.0 57.5 56.7 55.9

535 950 1134 1233

10 10

US-09-770-509-1
0 US-09-974-300-4664
0 US-09-974-300-180
0 US-09-9815-242-6542

Sequence 1, Appli Sequence 4664, Ap Sequence 180, App Sequence 6542, Ap

Description

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; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FASTSEQ for Windows Version (SEQ ID NO 4664)
; SEQ ID NO 4664
; LENGTH: 950
US-09-770-509-2 (1-178)
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                                                               Best Local Similarity:
                                                                             Percent Similarity:
                                                                                            Score:
                                                                                                            Pred. No.:
                                                                                                                            Alignment Scores:
                                                                                                                                                           US-09-974-300-4664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4664, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                         TYPE:
                                                                                                                                                                        ORGANISM: Bacillus.
                                                                                                                                                                                         DNA
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509.00
74.86%
57.71%
57.51%
 x US-09-974-300-4664 (1-950)
                                             Conservative: Mismatches: Indels:
                             Gaps:
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APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gen
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                    US-09-770-509-2 (1-178) x US-09-974-300-180 (1-1134)
                                                                                                             Query Match:
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                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 GGTTCTGATATGGTCTTTATTACTGCCGGAATGGGAGGAGGAACAGGCACCGGAGCAGCT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 CCAGAAATAGGCAAGAAAGCGGCAGAGGAAAGCAGAGAACAGCTGGAAGAAGTTCTTACA 282
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SerGlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArg
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74.01%
54.80%
56.72%
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Matches:
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TITLE OF INVENTION: IDENTIFY TO THE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRIOR DATE: 2000-11-26
PRIOR PRIOR DATE: 2000-12-26
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-26
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T
                 SOFTWARE: FastSEQ for Windows Ve
SEQ ID NO 6542
LENGTH: 1233
TYPE: DNA
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6542, Application US/09815242 Patent No. US20020061569A1
                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GluLeuAlaLysTyrValAspThrLeuTleValValProAsnGlnAsnLeuLeuAlaLeu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 CTGAAAGGTGCAGATATGGTGTTCGTCACAGCCGGAATGGGCGGCGGAACAGGAACGGGC
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217 GCCAATCCGGAAGTGGGCAAAAAAGCCGCAGAGGAAAGCCAAAGACAAATTGAAGAAAGCG
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-815-242-6542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3854, Application Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR ETLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                              APPLICANT:
                                                                                               CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (1)
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                                                                                                                                                                                                                                                                 Trawick, John D.
                                                                                                                                                                                                                                                                                       Wall, Daniel
                                                                                                                                                                                                                                                                                                        Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                       Xu, H. Howard
                                                                                                                                                                                                                                                Carr,
                                                                                                                                                                                                                        Yamamoto, Robert T
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Matches:
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RESULT 6
US-09-070-927A-128/c
Sequence 128, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecalis
TITLE OF INVENTION: Enterococcus NUMBER OF SEQUENCES: 982
                                                           APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                            164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 GCAGAAACAGTGATTCAATTAGGCCCCTAAATACACTCGTGGTTTAGGTGCCGGTTCACAA
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                                                                                                                                                                                                                                                                                                AAGAAAACGCCAATGCTTGAAGCATTTAGAGAAGCTGATAATGTATTACGTCAAGGTGTT
                                                                                                                                                                                                                                                                                                                     LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                                                                                                                                                                                                                                                                                                                                            AAAGAAAACGTTGATACACTATTAATTATCTCAAACAACCGCTTATTAGAAGTCGTTGAC
                                                                                                                                                                                                                                                                                                                                                                                              AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATTTAGTTTTGAAGGTCCAAAACGTGGTCGTTTTTGCCGCTGAAGGAATTGCCTTATTA
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 30 TELEFAX: (301) 30 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                27671 CCATTTAGTTTTGAAGGTCCAAAACGTGGTCGTTTGCNTGCTGAAGGAATTGCCTTATTA
                                                                                                                                                                        27791 GGCGCGGATATGATTTCATTACTGCTGGTATGGGTGGCGGAACTGGTACAGGTGCTGCG
                                                                                                                                                                                                                                                      27851 CCTGAAGTTGGCCAAAAAGCTGCAGAAGAAAGTGAACAAGTGATTTCAGAATCATTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 32768 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
                                        104 ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                         84 ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr
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731 CCAGTAGTTGCAAAAATCGCTAAAGAATTAGGCGCTTTAACAGTTGGTGTAGTAACTCGT
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                                                                                                                                                                                               ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kenley K. Hoover REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PB369
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Matches:
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Query Match: Best Local Score:

SEQ ID NO 3854 LENGTH: 1239

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PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/165,124

PRIOR APPLICATION NUMBER: 60/165,086

PRIOR APPLICATION NUMBER: 60/165,086

PRIOR FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 292

SOFTWARE: FastSEQ for Windows Version Type: DNA

Type: DNA

Type: DNA
                                                                                                                                                                                                                                                                            US-09-770-509-2 (1-178) x US-09-712-363-75 (1-1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-75
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PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR PRIOR PARTICIPATION NUMBER: 60/117,844
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR PILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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                                                             44 ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln 63
                                                                                                                                 24 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
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                          CTCAAAGGCGTGGAATTCATCGCGATCAACACCGACGCCCAGGCGTTGTTGATGAGCGAT 153
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                                                                                                              Application US/09712363
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485.00
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Matches:
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Publication No. US20030082657A1
GENERAL INFORMATION:
APPLICANT: Katagiri, F.
TITLE OF INVENTION: OMMYCETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES FILE REFERENCE: NADII.018A
CURRENT EILING DATE: US/09/770,509
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
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NAME/KEY: CDS
LOCATION: (2).
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                                                                                                                                                                                                                                                      21 ArgSerLeuAlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAla 40
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; ORGANISM: Staphylococcus
US-09-815-242-4715
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                                                                                                                                                                    Query Match:
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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LENGTH: 1172
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PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT APPLICATION NUMBER: 60/191,078
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                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
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                           INFORMATION
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                                                            LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu
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                                                                                                                        SEQ ID NO 8625
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes TILE REFERENCE: ELITRA.011A
                                                                                                                                           SOFTWARE:
                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-09 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
NAME/KEY: CDS
LOCATION: (1)...(1179)
                                         ORGANISM: Staphylococcus aureus FEATURE:
                                                                                 LENGTH: 1179
TYPE: DNA
                                                                                                                                                                                                                          APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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223 CCTGAAATCGGTAAAAAGCTGCAGAGGAATCTCGTGAACAATTGAAGATGCAATCCAA 282
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                                                                                                                                             FastSEQ
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Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
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US-08-781-986A-342
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                              Sequence 342, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: D1skette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTMARE: ASCIL Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
  PRIOR APPLICATION DATA:
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                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                            COUNTRY: U
ZIP: 20850
                                                                                                                                                                                                                                                 STATE: Maryland
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Best Local Similarity:
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                 Sequence 1, Application US/09754608
Patent No. US2002004580A1
GENERAL INFORMATION:
APPLICANT: Fueyo, Joanna Lynn
APPLICANT: Lonetto, Michael A.
APPLICANT: Pearce, Kenneth
TITLE OF INVENTION: ftsz
FILE REFERENCE: GM10068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3931 base pairs
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NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (301) 309-8504
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STRANDEDNESS: double
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RESULT 13
US-09-815-242-9381
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PRIOR APPLICATION NUMBER: 1998-07-22
PRIOR APPLICATION NUMBER: 60/055,720
PRIOR FILING DATE: 1997-08-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 1
ENCTH: 1260
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                                                                                                                                                     Sequence 9381, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                   GENERAL INFORMATION:
                                                                    APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
                                    APPLICANT:
APPLICANT:
                    APPLICANT:
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TYPE: DNA
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CURRENT FILING DATE: 2001-01-04
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                                                                                                                                                                                                                                                  592 ATTACCGATTTGATTACCAATCCAGGATTGATTAACCTT 630
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Yamamoto, Robert T
              Trawick, John D. Carr, Grant J.
                                                      Wall, Daniel
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; LOCATION: (1)...(1260)
US-09-815-242-9381
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Query Match:
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
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CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 12
TYPE: DNA
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                                    146 ThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuGluGlyValLysGly
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR ETLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/25968
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
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Best Local Similarity:
Query Match:
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US-09-738-626-2360
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TYPE: DNA
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                    124 AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
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                                                                                                                                                                                ProvalValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
                                                                                                                                                                                                                       GGCGCCGACATGGTCTTCGTTACCGCCGGCGAAGGTGGTGGCACCGGAACTGGTGCTGCA 333
                                                                                                                                                                                                                                                                                                    CCAGAAGTTGGACGTGCCTCGGCAGAGGATCACAAGAACGAAATCGAAGAAACCATCAAG
                                                            CCTTTCGAGTTCGAAGGCCGTCGCCGTACTCGCCAGGCAGAAGAAGGCATCGCAGCACTG
                                                                                                 ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu 123
                                                                                                                                           CCAGTCGTCGCCAGGGATCGCCAAGAAGATGGGCCGCACTGACCATTGGTGTTGTGACCAAG
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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OCHIAI, KEIKO
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Length:
Matches:
Conservative:
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Best Local Similarity:
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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US-09-738-626-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3309400
                      2279882
                                                                                                                                                                                                                                                           2280062 GCCGACGTAAAGCTCGATATCGGACGTGAAGCTACCCGTGGTCTTGGTGCCGGCGCGAAC 2280003
                                                                                                                                                                                                                                                                                                                                        2280122 CTCAAAGGCGTGGAGTTCATCGCGGTGAACACCGACTCGCAGGCTCTCATGTTCTCTGAT 2280063
                                                                                                   2279942
                                                                                                                                                                                2280002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 GCGAACCTGTCCATCATGGAAGCGTTCCGCGCAGCCGATGAAGTTCTCCACAATGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574 CAGGGTATTACCAACCTGATCACCATCCCTGGTGTGATCAACGTG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 AAGGAGGTCTGCGACACCCTCATCGTTATTCCAAACGACCGCCTGCTTGAGCTGGGCGAT 513
                                                            84
                                                                                                                                                                                                                   44 ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
                                                                                                                                                                                                                                                                                              24 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
                                                                                                                                                                                                                                                                                                                                                            4 LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu 23
                                       ProvalValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
                                                                                               GCGCCGACATGGTCTTCGTTACCGCCGGCGAAGGTGGTGGCACCGGAACTGGTGCTGCA
                                                                                                                  AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla 83
                    CCAGTCGTGGCAGGGATCGCCAAGAAGATGGGCGCACTGACCATTGGTGTTGTGACCAAG 2279823
                                                                                                                                                                              CCAGAAGTTGGACGTGCCTCGGCAGAGGATCACAAGAACGAAATCGAAGAAACCATCAAG 2279943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKEDA, MASATO
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Run

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Command line parameters:
-MODEL-frame+_p2n.model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL-frame+_p2n.model -DEV-x1h
-Q-/cgn2_1/USPT0_spool/US09770509/runat_27052003_083651_18863/app_query.fasta_1.327
-Q-/cgn2_1/USPT0_spool/US09770509/runat_27052003_083651_18863/app_query.fasta_1.327
-DB-Pending_Patents_NA_main -QFMT-fastap -SUFFIX=rnpm -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LOOPEXT=0 -THR_SCORE-pct -THR_MAX=-100 -THR_MIN=0 -ALIGN=15
-MODE=-LOCAL_GN=200 -THR_SCORE-pct -THR_MAX=-100 -THR_MIN=0 -MAXLEN=2000000000
-MODE=-LOCAL_CN-CNC - NORM-ext - HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09770509_@CGN_1_1_2950_@runat_27052003_083651_18863 -NCPU=6 -ICPU=3
-NC_XLPXY -NO_MANP_-LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-EGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xgapop 10.0
Ygapop 10.0
Ygapop 6.0
Fgapop 6.0
Delop 6.0
   US-09-770-509-2
885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24791104 segs, 12571243825 residues
   I: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*

/cgn2_6/ptodata/1/pna/US080_COMB.seq:*

/cgn2_6/ptodata/1/pna/US081_COMB.seq:*

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/cgn2_6/ptodata/1/pna/US086_COMB.seq:*

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/cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/pna/US06_COMB.seq:*
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1634.537 Million cell updates/sec
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cgn2_6/ptodata//pna/US6034_COMB.seq:
cgn2_6/ptodata//pna/US6034_COMB.seq:
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/cgn2_6/ptcodata/1/pna/US097C_COMB.seq;
/cgn2_6/ptcodata/1/pna/US098A_COMB.seq;
/cgn2_6/ptcodata/1/pna/US098B_COMB.seq;
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/cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
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)ptodata/1/pna/US100A_COMB.seq:*
)/ptodata/1/pna/US101A_COMB.seq:*
)/ptodata/1/pna/US101A_COMB.seq:*
)/ptodata/1/pna/US101B_COMB.seq:*
//ptodata/1/pna/US101B_COMB.seq:*
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/ptodata/1/pna/US099C_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Length DB ID	Bd	ID	Description
1		100.0	) 535	30	100.0 535 30 US-09-770-509-1	
2	550	62.1	147:	38	US-10-015-127-5607	
ი ა	550	62.1	2474	38	US-10-015-127-522	
4	509	57.5	95	36	US-09-974-300-4664	
ი 5	509	57.5	207	71	US-60-279-526-159	
σ	506	57.2	11130	ч	PCT-US98-12764-3	Sequence 3, Appli

o o

12 40

181 60

241

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APPLICANT: Katagiri, F.
TITLE OF INVENTION: OON/CETE FTSZ-MT AS A TARGET FOR TITLE OF INVENTION: ANTIMICROBIAL-SPECIFIC BIOCIDES FILE REFERENCE: NADII.018A
CURRENT APPLICATION NUMBER: US/09/770,509
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 535
TYPE: DNA
ORGANISM: Phytophthora infestans
                           Best Local Similarity:
Query Match:
DB:
  US-09-770-509-2 (1-178) x
                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                           US-09-770-509-1
: Sequence 1, Application US/09770509
: GENERAL INFORMATION:
                                                               Percent Similarity:
                                                                                                                            us-09-770-509-1
                                                                                                                                    NAME/KEY: CDS
LOCATION: (2)...(535)
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885.00
100.00%
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 US-09-770-509-1 (1-535)
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PCT-US02-03987-4715
US-09-815-242-4715
US-10-072-851-4715
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                                    Matches:
Conservative:
Mismatches:
Indels:
                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Appli
Sequence 4715, Ap
Sequence 4715, Ap
Sequence 4715, Ap
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Sequence 1, App
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                                     Вþ
                                                           Qy
                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Sphingomonas elodea
US-10-015-127-5607
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US-10-015-127-5607
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Best Local Similarity:
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SEQ ID NO 5607
LENGTH: 1473
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5607, Application US/10015127 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences
FILE REFERENCE: 38-10(15806)B
FILE REFERENCE: 38-10(15806)B
CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR PILING DATE: 2000-11-22
                                                                                                                                                                           No.:
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81 GlyAlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyVal 100
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                                                 SerGlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArg
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US-10-015-127-522/c
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GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof FILE REFERENCE: 38-10(15806)B
CURRENT APPLICATION NUMBER: US/10/015,127
CURRENT FILING DATE: 2001-10-29
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
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SEQ ID NO 522
LENGTH: 24740
TYPE: DNA
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y Match:
                                                                                                                   3426 TCGGTTGCGCCGCAGCGCATTCAGCTGGGCGCGAAGATCACGCAGGGCCTGGGCGCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 SerThrProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLys
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                                                                               42 SerLysProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMet
                                                                                                                                       22 SerLeuAlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGly 41
                                                                                                                                                                                                                   2 SerGlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGTGCGCGGCATCACCGACCTGATGGTGATGCCCGGCCTGATCAACCTC 636
                                          TCGCGGCCCGAAATCGGCCGTGCGGCGGCCGAGGAGGACGATCGAGCAGGTCCAGCAGTCG
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APPLICANT: Clausen, Ib Groth
APPLICANY: Clausen, Ib Groth
ITTLE OF INVENTION: Methods For Monitoring Mu
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION UMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER: TING APRIOR FILING DATE: ARA
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Best Local Similarity:
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LENGTH: 950
TYPE: DNA
ORGANISM: Bacillus
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                4 LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu
                                                            AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla 83
                                                                                                                                                                                              GCGGAAAAGAAGTTGCAACTTGGCGGCAAACTTACTCGCGGCCTTGGCGCTGGCGCCAAC 222
                                                                                                                                                                                                                                                                           CTGCAAGGTGTTGATTTTATTGCAGTCAATACAGATGCACAAGCACTCCATTTATCAAAA 162
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  ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
                                        GGTTCTGATATGGTCTTTATTACTGCCGGAATGGGAGGAGGAACAGGCACCGGAGCAGCT
                                                                                                                   CCAGAAATAGGCAAGAAAGCGGCAGAGGAAAGCAGCAGCTGGAAGAAGTTCTTACA 282
                                                                                                                                                        ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln 63
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US-60-279-526-159/c
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; ORGANISM: B. clausii
US-60-279-526-159
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 159
LENGTH: 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 159,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sorokine, Alexei
APPLICANT: Bolotine, Alexandre
APPLICANT: Lapidus, Alla
TITLE OF INVENTION: Methods For Monitoring Multiple
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Expression
FILE REFERENCE: 5963.000-US
CURRENT APPLICATION NUMBER: US/60/279,526
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 2232
SOFTWARE: FastSEQ for Windows Version 4.0
           104 ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu 123
                                                         617
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                                                                                                                                                                                                           737
                                                                                                                                                                                                                                                                                                                                                 857 CTGCAAGGTGTTGATTTATTGCAGTCAATACAGATGCACAAGCACTCCATTTATCAAAA 798
                                                                                                                                                                                                                                                                                    797
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                                                                                                                                               64 AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla 83
                                                                                                                                                                                                                                    44 ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln
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                                                                                                                                                                                                                                                                                               24 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
                                                                                                                                                                                                                                                                                                                                                                    4 LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu
                                                                                                                          GGTTCTGATATGGTCTTTATTACTGCCGGAATGGGAGGAGGAACAGGCACCGGAGCAGCT 618
                                                   ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
                                                                                                                                                                                                                                                                            GCGGAAAAGAAGTTGCAACTTGGCGGCAAACTTACTCGCGGCCTTGGCGCTGGCGCCAAC 738
                                                                                                                                                                                                     CCAGAAATAGGCAAGAAAGCGGCAGAGGAAAGCAGGAAGAACAGCTGGAAGAAGTTCTTACA 678
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Best Local Similarity:
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                                                                                                                                                                                                                  Query Match:
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PCT-US98-12764-3
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GENERAL INFORMATION:
APPLICANT: Gil Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Borrelia burgdorferi Polynucleotides and Sequences NUMBER OF SEQUENCES: 155
                                                                                                                                                                                                                                                                                             No : :
                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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           13007 AAAATTGCCCTTGGAGCAAAAGTTACAGCAGGGCTTGGTGCTGGGGGGAAAGCCTGAGATT 13066
                                                                                12947 GTTGAATTTATTGTGGCTAATACCGATCTTCAGGCTCTCCAAACTTCTATTGCTCCCATA 13006
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                            27 LysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLysProGluLeu 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497 AAAGAAAAAGTGGACACATTGATCGTGATTCCAAATGACCGCTTATTGGAAATGGTTGAT 438
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                                                                                                       7 ValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeuAlaProHis 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20850
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9410 Key West Avenue
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HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                    linear
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Matches:
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Alignment Scores:  4.92e-41 Length: 111309 Score: 506.00 Matches: 101		; SEQUENCE CHARACTERISTICS: ; LENGTH: 111309 base pairs ; TYPE: nucleic acid	TELEPHONE: (301) 309-8512  INFORMATION FOR SEQ ID NO: 3:	NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB370PCT	PRIOR APPLICATION UNMER: PCT/US98/12764  FILING DATE: <unknown>  ATTORNEY AGENT INFORMATION.</unknown>	FILING DATE: 24-Apr-2001 CLASSIFICATION: <unknown></unknown>	MEDIUM TYPE: Diskette, 3.50 Inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA.	and FORM:		INFORMATION: PLICANT: G11 CH TTLE OF INVENTIC	RESULT 7 US-09-830-228-3 ; Sequence 3, Application US/09830228	Qy 167 ThrAspLeuIleValArgProGlyLeuIleAsnLeu 178	Qy 147 ThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyValLySGlyVal 166			QY 87 AlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThrProPheArg 106	Qy 67 MetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAlaProValVal 86     :::	Qy 47 GlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGlnAspSerAsn 66     :::
	; CLESSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: ; ETLING DATE: . ATTO DENEY AGENT INFORMATION.	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: PCT/US98/12764 ; FILING DATE: Herewith CIASSITETATION:	; MEDIUM TIPE: DISKETTE, 3.30 INCH, 1.4MD STORAGE; COMPUTER: HP Vectra 486/33; OPERATING SYSTEM: MSDOS version 6.2; SOFTWARE: ASCII Text	UNTRY: USA  IP: 20850  PUTER READABLE FORM:	; ADDRESSEE: Human Genome Sciences, Inc. ; STREET: 9410 Key West Avenue ; CITY: Rockville	; APPLICANT: GIL CHOI Et. al. ; TITLE OF INVENTION: Borrella burgdorferi Polynucleotides and Sequences ; NUMBER OF SEQUENCES: 155 ; CORRESPONDENCE ADDRESS:	1 pplication PC/ RMATION:	Qy 167 ThraspLeuIleValArgProGlyLeuIleAsnLeu 178	Qy 147 ThrmetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyValLysGlyVal 166    :::  ::     :::	Qy 127 ValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSerThr 146	Qy 107 SerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLysTyr 126	AlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThrProPheArg	Qy 67 MetLeubhelleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAlaProValVal 86    :::	Qy 47 GlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGlnAspSerAsn 66	Qy 27 LysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLysProGluLeu 46	Oy ValGiubheileValAlaAshThrAspCysGinAlaLeuGlyArgSerLeuAlaProHis 26	770-509-2 (1-178) x US-09-830-228-3 (1-111309)	Percent Similarity: 74.42% Conservative: 27 Best Local Similarity: 58.72% Mismatches: 44 Query Match: 57.18% Indels: 0 DB: 32 Gaps: 0

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US-09-830-228-1
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                                                                                                                                                                                                       Sequence 1, Application US/09830228 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 910715 base pairs
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TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Мо.:
                                                                                                                                                                                                                                                                                       602813 GCAGGGCTTATTATTGAGCATGGAGAGGTTAATATT 602848
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 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                               APPLICANT: Gil Choi et. al.
TITLE OF INVENTION: Borrelia burgdorferi Polynucleotides and Sequences
NUMBER OF SEQUENCES: 155
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                                  ZIP: 20850
                                                                                       CITY: Rockville
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Best Local Similarity:
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 10
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LENGTH: 910715 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                               147 ThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyValLysGlyVal
                                                                                                                                                                                   127 ValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSerThr
                                                              167 ThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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                                 GCAGGGCTTATTATTGAGCATGGAGAGGTTAATATT 602848
                                                                                                                                                                                                                                                                SerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLysTyr 126
                                                                                                                                                                                                                                                                                                   AlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThrProPheArg
                                                                                                                                                                                                                                                                                                                                                                       ATGGTGTTTATTACTGCTGGTATGGGGGGGGGGACAGGAACCGGAGCAGCTCCAGTTATT
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB370PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/830,228 FILING DATE: 24-Apr-2001 CLASSIFICATION: <Unknown>
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING
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RESULT 11
US-09-754-468-42
; Sequence 42, Application US/09754468
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Cell;
TITLE OF INVENTION: Composition and Method
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US-09-663-779-1189
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LENGTH: 7375
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/663,779
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/154,678
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 8283
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APPLICANT: Malvar, Thomas M.
APPLICANT: Shukla, Hridayabhiranjan
TITLE OF INVENTION: BACILLUS THURINGIENSIS
TITLE OF INVENTION: THEREOF
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                                                                                                                                                                                                                                                        144 LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                                                                                                                     164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyThrCysThrGlyAlaAla
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                                                                                                                                                                                                                          AAAAATACGCCAATGTTAGAAGCATTCCGTGAAGCTGATAACGTATTACGTCAAGGTGTT
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Query Match:
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 APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Mu
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION UMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                        US-09-974-300-180
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                                                                                                                                                                                     Sequence 180, Application US/09974300 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: US 60/174,484
PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 112
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TYPE: DNA
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                                                                                                                                                                                                                         Sequence 854, Application US/60045649 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 180
LENGTH: 1134
TYPE: DNA
ORGANISM: Bacillus licheniformis
                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                         APPLICANT: Lagace, Robert E.
APPLICANT: Corely, Neil C.
APPLICANT: Russo, Frank D.
APPLICANT: Hann, Amy L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1466
               COUNTRY:
                            STREET: 3174 POI
CITY: PALO ALTO
STATE: CALIFORN:
                                                                                                                                                                                                                                                                                                      577 GGTGTTCAGGGCATTTCAGACCTGATCGCAACGCCTGGACTGATCAACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAAAGCGGAAACGAAAATGCAGATCGGTGCGAAGCTGACGCGCGGGCTCGGCGCCGGA 216
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                              CALIFORNIA
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Mismatches:
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TELEFAX: (415) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cD
IMMEDIATE SOURCE:
CLONE: EF1c0854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM
TELECOMMUNICATION INFORMATION:
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NAME: CERRONE, MICHAEL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                         3067
                                                                                                                                                                                                     3007 CCATTTAGTTTTGAAGGTCCAAAACGTGGTCGTTTTGCCGCTGAAGGAATTGCCTTATTA
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                                 164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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          CAAGGGATTTCAGATTTAATCACTGCACCAGGTTACGTAAACTTA 3231
                                                                       AAGAAAACGCCAATGCTTGAAGCATTTAGAGAAGCTGATAATGTATTACGTCAAGGTGTT
                                                                                                LysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyVal 163
                                                                                                                                       ANAGAAAACGTTGATACACTATTAATTATCTCAAACCAACCGCTTATTAGAAGTCGTTGAC
                                                                                                                                                                   AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp
                                                                                                                                                                                                                       ProPheArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeu
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                                                                                                                                                                                                                                                                                                                                  GCGCGGATATGATTTCATTACTGCTGGTATGGGTGGCGGAACTGGTACAGGTGCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEPAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 853:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 853, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/60/046,653
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COTIEY, Neil C.
APPLICANT: Russo, Frank D.
APPLICANT: Hann, Amy L.
APPLICANT: Heath, Joe D.
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Sir
TOPOLOGY: linear
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                                     2887 GGCGCGGATATGATTTCATTACTGCTGGTATGGGTGGCGGAACTGGTACAGGTGCTGCG
                                                                                                           2707 GTTAAAGGCGTGGAATTTATCACAGCCAATACAGACGTTCAAGCATTAAAACATTCAAAA 2766
                                                                   64 AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla
                                                                                                                                             44 ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln 63
                                                                                                                                                                                                    24 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
                                                                                                                                                                                                                                                                           94304
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 ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
PCT-US02-03987-6542
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6542
LENGTH: 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6542, Application PC/TUS0203987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Methods for Identities OF INVENTION: Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Elitra Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                      ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
                                                                                                         GGCGCGGATATGATTTTCATTACTGCTGGTATGGGTGGCGGAACTGGTACAGGTGCTGCG
                                                                                                                                             AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla
                                                                                                                                                                                 CCTGAAGTTGGCCAAAAAGCTGCAGAAGAAAGTGAACAAGTGATTTCAGAATCATTACAA
                                                                                                                                                                                                                                                                           AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
                                                                                                                                                                                                                                                                                                                                                            LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu 23
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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh
-Q-Ggn2_1/USBTO_spool_VE09770509/runat_27052003_083652_18961/app_query.fasta_1.327
-Q-Ggn2_1/USBTO_spool_VE09770509/runat_27052003_083652_18961/app_query.fasta_1.327
-DB-Pending_Patents_NA_New -QFMT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-NODE=LOCAL -OUTFMT=Pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=16 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptcdata/1/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptcdata/1/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptcdata/1/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptcdata/1/pna/US09_NEW_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
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    8 US-10-398-221-2058
US-10-282-122A-15434
US-10-282-122A-10897
US-10-282-122A-10662
US-10-282-122A-9479
                                                                                                                       US-10-282-122A-24440
US-10-398-221-6
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Sequence 24440, A
Sequence 6, Appli
Sequence 2058, Ap
Sequence 15434, A
Sequence 10897, A
Sequence 10662, A
Sequence 9479, Ap
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	-282-122A-38	-366-683-778	-419-128-778	-366-683-755	-419-128-7557	-282-122A-3	-282-122A-4031	-057-498-104	-978-825-10	502-32727-10	US-10-282-122A-33518	-282-122A-3172	-282-122A-3792	-950-084-7442	-329-624-342	0-009-861-19	-092-411A-1997	-282-122A-34	-282-122A-782	-950-084-1797	-282-122A-2760	-282-122A-35	-282-122A-2846	-282-122A-2615	)-156-761-1	-282-122A-17	-156-761-6101	JS02-36123-6	502-36123-520	302-36122-83	-282-122A-16	-282-122A-2578	S-10-282-122A-2140	S-10-417-884-3641	S-09-134-000C-125	S-09-134-000	-10-282-122A-628	-10-282-122A-171
•	equence 38466,	equence 7784, A	equence 7784, A	equence 7557, A	equence 7557, A	equence 30463	equence 40313,	equence 104, Ap	equence 104, Ap	equence 104,	3351	equence 3172:	equence 37929	equence 7442	equence 342,	Sequence 190	equence 1997	equence 34541	7824	equence 1797	2760	equence 3532;	2846	26150	ж 1, 1	1783	6101,	665	5201	83	16538	2578	2140	3641	1253	Sequence 1253, Ap	6285	1714

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## ALIGNMENTS

US-10-282-122A-24440

Sequence 24440, Application US/10282122A GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Zyskind, Judith Ohlsen, Kari

Daniel

APPLICANT:

APPLICANT:

Zamudio, Cario Malone, Cheryl

Carlos

Liangsu

Haselbeck, Robert

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APPLICANT:
                              PRIOR PRIOR
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                                                                                                                                                                                  FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                     APPLICANT:
                                                                 PRIOR
                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                         APPLICANT:
                                                                               FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/
FILING DATE: 2000-05-26
                              APPLICATION NUMBER: 60/230,347
                                                                 APPLICATION NUMBER: 60/230,335
APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                   Forsyth, R.
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                 2000-09-09
                                                                                                                                                                                                                                                                                       Robert
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RESULT 2
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                      Sequence 6, Application US/10398221 GENERAL INFORMATION:
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             APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome
FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Listeria
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NUMBER: US/10/398,221
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RESULT 3
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                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
                                                                                                                                                                                                                                                                     Sequence 2058, Application US/10398221
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PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
                                                                                          TITLE OF INVENTION: Listeria innocua, genome FILE REFERENCE: 344 702 - US CURRENT APPLICATION NUMBER: US/10/398,221 CURRENT FILING DATE: 2003-03-27
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PRIOR APPLICATION NUMBER: PCT/FR 01/03
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
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ORGANISM: Listeria
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; ORGANISM: Listeria
US-10-398-221-2058
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                                                                                                                APPLICANT: Wang, I
APPLICANT: Zamudi
APPLICANT: Malone
APPLICANT: Haselt
APPLICANT: Ohlsen
APPLICANT: Zyskin
APPLICANT: Wall,
APPLICANT: Wall,
APPLICANT: Trawic
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SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2058
LENGTH: 3011208
                                                   APPLICANT:
               TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITRA.034A
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   REFERENCE: ELIT
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|CTTGAAATTGGTAAAAAGCAGCAGAAGAAGTCGCGAACAAATTGAAGAAGCTTTAAAA 2161666
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                                                                                                                                                                              Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                   Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                  Carr, Grant
                                                                                    Yamamoto,
                                                                                                                   Trawick, John
                                                                 Forsyth, R.
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR PPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PRICING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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SEQ ID NO 15434
LENGTH: 1122
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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ORGANISM: Borrelia
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PRIOR FILING DATE: 2000-09-06
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/267,636
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SEQ ID NO 10662
LENGTH: 1158
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APPLICANT: Zamud
APPLICANT: Malon
APPLICANT: Hasel
APPLICANT: Ohlse
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APPLICANT:
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                Remaining Prior Application data NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                  PRIOR FILING DATE: 2001-02-16
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            ORGANISM: Bacillus anthracis
                                TYPE: DNA
                                                                                                                                                                   APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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Malone, Cheryl
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APPLICANT:
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-23 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                        Carr, Grant
Yamamoto, Ro
Forsyth, R.
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Trawick, John
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Zyskind, Judith
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Malone, Cheryl
Haselbeck, Robert
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US-10-282-122A-17147 ; Sequence 17147, Application US/10282122A ; GENERAL INFORMATION:
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ORGANISM: Bacillus
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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US-10-282-122A-17147
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

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LENGTH: 1182
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PRIOR APPLICATION NUMBER: 60/253,625
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                                                      SerLysProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMet 61
                                                                                       LeuGlnAspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyThrCysThrGly 81
                   AlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValVal 101
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Zamudio, ca.
Cheryl
   Forsyth, R.
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Query Match:
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LENGTH: 1230
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GENERAL INFORM
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-05-26
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TITLE OF INVENTION: Identification of Essential Genes
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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APPLICATION NUMBER: 60/230,347
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Malone, Cheryl
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                                                                      US-09-770-509-2 (1-178) x US-09-134-000C-1253 (1-1308)
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APPLICANT: LYND DOUCETTE-Stamm et al
APPLICANT: LYND DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 1253
LENGTH: 1308
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
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                                                                                                                           Local Similarity: y Match:
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586 CAAGGGATTTCAGATTTAATCACTGCACCAGGTTACGTAAACTTG 630
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                  LeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeu 23
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US-09-134-000C-1253
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SEQ ID NO 1253
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APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: ENTERCOCOCUS FAECALIS FILE REFERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecalis
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                44 ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln
                                                                                   24 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AspSerAsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAla 83
                                                                                                                                          ProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThr 103
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US-10-417-884-3641
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                                                                                                                                                INFORMATION FOR SEQ ID NO: 3641:
SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
    HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                               TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/417,884 FILING DATE: 17-Apr-2003 PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THI
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TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAAAACGCCAATGCTTGAAGCATTTAGAGAAGCTGATAATGTATTACGTCAAGGTGTT
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                                                                                                           STRANDEDNESS: double
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                                                                                                                                                                                                                  TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTC-012
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      SOURCE:
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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; Sequence 21408, Application U;
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu;
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert;
; APPLICANT: Hoselbeck, Robert;
; APPLICANT: Ohlsen, Kari
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TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELLTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                        Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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                                                                                                                                                Carr, Grant
                                                                                                                                                                         Trawick, John
                                                                                                                               Yamamoto,
                                                                                                                                                                                                                                                          Haselbeck, Robert
                                                                                                       Forsyth, R.
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Best Local Similarity:
Query Match:
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PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-12-22
PRIOR FILLING DATE: 2000-12-267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
PRIOR FILLING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21408
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/230,335
                                                 164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu :::|||:::::||||||||||
                                                                                                                        466 AAAGAAAATGTGGATACATTATTAATTATCTCAAATAACCGTTTATTAGAAGTTGTAGAT
                                                                                                                                                           124 AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                              44 ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln
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TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25784
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITRA.034A
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FILING DATE: 2000-12-22
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FILING DATE: 2000-10-23
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                CCCGAGGTCGGCCGCAAGGCCGCCGAGGACGCCAAGGACGAGATCGAGGAGCTGCTGCGC
                                              ProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMetLeuGln
                                                                                 AlaProHisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLys 43
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Zyskind, Jud
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Forsyth, R.
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-29
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
                                                                     Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16538
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELLTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING DATE: 2003-02-20
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PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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         TYPE: DNA ORGANISM: Clostridium botulinum
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583 CAAGGTATATCAGATTTGATTACTATACCAGGACTTGTTAATTTA
                           164 LysGlyValThrAspLeuIleValArgProGlyLeuIleAsnLeu 178
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                                                                                                                  AAAGAGAGAGTAGACACTTTAGTTACAATCCCAAATGAAAGATTATTAAGTATAGTAGAT 522
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Search completed: June 2, 2003, 12:26:29

Job time : 5481 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh
-Q-/cgp2_1/USBTQ_gpool/USB99770509/runat_27052003_083649_18832/app_query.fasta_1.327
-DB-EST -QFMT-fastap -SUFFIX-rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blts -START=1 -END--1 -HARIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_WIN-0 -ALIGN-15 -MODE-LOCAL
-OUTEMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09770509_@CGM_11_11906_grunat_270752003_03549_18832 -NCPU-6 -ICPU-3
-NO_WMAP -LAREQUERY -NEG_SCORES-0 -MAXLEN-200000000
-USD-TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AI775094	RESULT 1
1 (bases 1 to 570)	ASTETIDAE; euasterids 1; Solanales; Solanaceae; Solanum; Lycopersicon.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Lycopersicon esculentum	tomato.	EST.	AI775094.1 GI:5273135	AI775094	clone cLER14D3, mRNA sequence.	EST256194 tomato resistant, Cornell Lycopersicon esculentum cDNA	AI775094 570 bp mRNA linear EST 18-MAY-2001		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Clemson University Genomics Institute
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100 Jordan Hall, C
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                                                                                    AACTTCAGAGAAATGTTGACACACTTATAGTAATTCCCAATGATCGTCTGCTAGATATT
                                                                                                  GluLeuAlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeu ::::||| ::: |||||| :::
                                                                                                                                                                                                                                                      GCCGATGAGCAGACACCACTTCAAGATGCTTTTCTTTGCGGATGATGTATTACGTCAA
                                                        AlaAspLysSerThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGlu
                                                                                                                                                                                                GCGGCTCCTGTTGTGGCTCAAATAGCAAAGCAGGTTATTTGACTGTTGGTGTTGTT
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/lab_host="SOLR"
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/tissue_type="leaf"
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/db_xref="taxon:4081"
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                                              GCTGCTCCAGTTGTTGCCCAGATATCAAAGGAAGCTGGTTATCTTACTGTTGGTGTTGTC
                                                                    AlaAlaProValValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValVal
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/db_xref="MaizeDB:631962"
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/clone="CL421_1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ578606 668 bp mRNA linear EST 19-JUN-2002 WHE0307_E03_J05ZS Wheat unstressed seedling shoot cDNA library Triticum aestivum cDNA clone WHE0307_E03_J05, mRNA sequence.
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The structure and function of the expressed portion of the wheat
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Tel: 5105595773
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Site_1: ECORI; Site_2: XhoI; Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Shoots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."

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                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Schulman AH
Institute of Biotechnology
University of Helsinki
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/tissue_type="Callus"
/note="Callus K19"
                                                     /clone="S0000800253A03F1"
/clone_lib="S00008"
                                                                                                              /organism="Hordeum vulgare"
/db_xref="taxon:4513"
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.33%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GAATCAAAGGAAGTGATAGCCAATGCCCTCCGAGATTCGGACCTTGTCTTCATAACAGCT
genomes - rac | Unpublished (2000)
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
US Department of Agriculture, Canter
West Area, Western Regional Research Center
Company Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 GlyMetGlyGlyThrCysThrGlyAlaAlaProValValAlaSerValAlaArgGlu 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 GlnGlnLysValAspIleGlnArgMetLeuGlnAspSerAsnMetLeuPheIleThrGly 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 CAATTGACTCGTGGGCTGGGTACTGGTGGAAATCCTAATTTGGGAGAACAGGCTGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 AspIleThrLysGlyLeuGlyAlaGlySerLysProGluLeuGlyLysArgSerAlaGlu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                          1 (bases 1 to 593)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE498211 593 bp mRNA linear EST 04-AUG-20 WHE0954_C01_F02ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0954_C01_F02, mRNA sequence.
                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooides; Triticeae; Triticeum.
                                                                                                                                                                                                                                                                                                                                     bread wheat.
Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLysTyrValAspThrLeuIleVal 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGlyFleLeuThrValGlyValValSerThrProPheArgSerGluGlyProAsnArg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACACAGATTCCCAGGCTCTCGTCAATTCGCAGGCACAACATCCGTTACAAATTGGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCTTGCAGATGATGTCCTTCGTCAGGGTGTCCAAGGAATATCAGACATAATCACGATA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACCAAATGATCGGTTGTTAGATATTGCTGATGAAAATATGCCCTTGCAAGACGCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTACAGGCACTTGAAGCATTAGAGAAGCTGGAAAGGAGTGTTGACACACTAATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match:
                                                           166 ValThrAspLeuIle 170
                                                                                                      450 ATGCCCTTGCAAGACGCGTTTCTCCTTGCAGATGATGTCCTTCGACAGGGTGTCCAAGGA
                                                                                                                                                                                          390 AGTGTTGACACTCTGATTGTGATCCCAAATGATCGGTTGTTAGATATTGCTGATGAGAAT
                                                                                                                                                                                                                                   126 TyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSer 145
                                                                                                                                                                                                                                                                                 330 AGCTTTGAAGGACGCAAGCGCTCTCTACAGGCACTCGAAGCATTGGAGAAGCTGGAAAGA
                                                                                                                                                                                                                                                                                                                                                                       270
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                                                                                                                                                                                                                                                                                                                       106 ArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLys 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 AsnMetLeuPheIleThrGlyGlyMetGlyGlyGlyThrCysThrGlyAlaAlaProVal
                                                                                                                                                                                                                                                                                                                                                                                                              86 ValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThrProPhe 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 HisLysIleThrLeuGlyLysAspIleThrLysGlyLeuGlyAlaGlySerLysProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GGTATCGAGTTTTATGCTATAAACACAGATTCCCAGGCTCTTGTGAATTCGCAGGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
Sequence have been trimmed score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSerLeuAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence with phred score less than seq primer: Stratagene SK primer.
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                                                                                                                                 ThrThrMetLeuGluAlaPheArgTyrAlaAspAspValLeuLeuGluGlyValLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli_SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="WHE0954_C01_F02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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1 311 c 404 g 374 t 96 others
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/db_xref-"MaizeDB:632908"
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ESTs from leaves of Medicago truncatula after inoculation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae; Trifolleae;
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Fax: 651 649 5058
Email: debbys@puccini.crl.umn.
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Department of Plant Pathology
University of Minnesota
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Unpublished (2000)
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EST335027 DSIL Medicago
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                                      /dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii" /lab_host="E. coli strain XLOLR" /lab_host="E. coli strain XLOLR" /note="vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were exclsed from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."
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/db_xref="taxon:3880"
/clone="pDSIL-3J17"
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trifolii"
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1024043F01.y2 C. reinhardtii CC-1690, normalize
Chlamydomonas reinhardtii cDNA, mRNA sequence.
BG855721
BG855721.1 GI:14236905
EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
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                                                                                                                                             Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulat Vascular Plants; project phase 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 SerLysProGluLeuGlyLysArgSerAlaGluGlnGlnLysValAspIleGlnArgMet
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 Email: chauser@duke.edu.
Location/Qualifiers
                                    Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                     Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
                                                                                                                                                                                                                                                       Chlamydomonadaceae; Chlamydomonas
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EST287730 tomato
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tomato
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                                                             cLET29K5, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript II SK-; Site_1: EcoRI;
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404.00
68.75%
51.88%
45.65%
                                                                            670 bp mixed elicitor,
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664 83 27 48

BTI Lycopersicon esculentum cDNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: CUGI
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                                                                                       TyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAspLysSer
                                                                                                                          TCTTTTGAGGGACGAAGAAGAGCAGTTCAAGCCCAAGAAGGAATTGCAGCTTTGAGAGAA
                                                                                                                                                              ArgSerGluGlyProAsnArgThrArgLeuAlaAsnAlaGlyValLysGluLeuAlaLys 125
                                                                                                                                                                                                                                 ValAlaSerValAlaArgGluLeuGlyIleLeuThrValGlyValValSerThrProPhe 105
                                                                                                                                                                                                                                                                      GATATGGTTTTTGTGACTGCTGGAATGGGCCGGAGGAACAGGGACTGGTGGGGCTCCTATA 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="4-6 week old plants"
/dev_stage="4-6 week old plants"
/lab_host="xL1-Blue MRF',"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone-"cLET29K5"
/clone_lib-"tomato mixed elicitor,
/tissue_type-"leaf"
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/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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US-09-770-509-2 (1-178) x BJ289183 (1-621)
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                                                                                                                                                                   35 ThrLysGlyLeuGlyAlaGlySerLysProGluLeuGlyLysArgSerAlaGluGlnGln
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BJ289183
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TGTGAGTCCATAGAGGAAGCACTTCATGGTGCTGACATGGTTTTTGTCACGGCAGGAATG 139
                                                   LysValAspIleGlnArgMetLeuGlnAspSerAsnMetLeuPheIleThrGlyGlyMet 74
                                                                                                             ACTCGGGGTCTGGGTGCGGGTGGGAACCCTGATATTGGGATGAATGCTGCCAAGGAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Site_1: ECORI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown unde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Y. Ogihara unpublished cDNA library, Wh_SL"
/tissue_type="seed DPA30"
/dev_stage="Feekes' scale 11.3"
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/clone="who?3-17"
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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615 bp mRNA linear EST 07-MAR-20
BJ361253 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddcl6n12 5', mRNA sequence.
BJ361253
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Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-1, T.
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CTGGTTAATGTT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGATGATATTCTTTGGCAAGGAATTCGCGGTATCTCTGATATCATTACGGTTCCTGGG 439
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                                                                                                                                                                                                                                                                                      /db_xref="taxon:44689"
/clone="ddc16n12"
/clone_lib="Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                        /strain="AX4"
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 241 GAATTATATGGAATTGATTTTGTAGTTGCCAATACTGATGCACAAGCATTGGCAATATCA
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Tadasu Shin-i
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Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-1,T.
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                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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             GlnLeuGluGlyValGluPheIleValAlaAsnThrAspCysGlnAlaLeuGlyArgSer
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/clone="ddv23d18"
                                                                                                                                                                                                                                                                       /clone_lib="Dictyostelium
/sex="mat A"
                                                                                                                                                                                                                                                                                                                                        /strain="AX4"
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Maize ESTs from various cDNA libra
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
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Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                 walbot@stanford.edu
1091033 row: D colu
Location/Qualifiers
                                                                                                                                          /lab_host-"Stratagene XLOLR"
/note-"Organ: Immature ear; Vector: pAD-GAL4;
ECORI; Site_2: Xhol; RNA from library 606 was
common ESTs found in 606."
                                                                                                                                                                                                                         /tissue_type="Inflorescence meristem
primordia"
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/clone_lib="1091 - Immature ear with
                                                                                                                                                                                                                                                                                                      /organism-"Zea mays"
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                                                                                                                                                                       Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                  Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
                                                                                                                                                                                                                                                                                                                                                                             Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig7869, see http://cgpdb.uc
for details.
                                                                                                                                           Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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te: QGJ1 row: M
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/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
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                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                               BQ869798 765 bp mRNA linear EST 15-AUG-200
QGD7D11.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
QGD7D11, mRNA sequence.
BQ869798
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellis, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                                                       Lactuca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for details.
Plate: QGD7
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belongs to contig QG_CA_Contig7869, see http://cgpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
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                                                                              GAGCAGACACCCCTTCAGGATGCTTTTCTTCTTGCTGATGATGTACTCCGTCAAGGCGTT
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                                                                                                                                                                                      AlaLysTyrValAspThrLeuIleValValProAsnGlnAsnLeuLeuAlaLeuAlaAsp ::: ||||||| :::||||||
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//lab_host="E.coli"
//lab_host="E.coli"
//note="Vector: pBBcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QG_ABCDI lettuce salinas
TAG_TISSUE=chemical induction
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/cultivar="Salinas"
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